



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165896

TO: Nita M Minnifield
Location: REM/3C01/3C18
Art Unit: 1645
Saturday, September 17, 2005

Case Serial Number: 10/002784

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

*Reviewed
9-05*

THIS PAGE BLANK (USPTO)

STIC-Biotech/ChemLib

165896

From: Minnifield, Nita
Sent: Thursday, September 15, 2005 4:51 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

10/002784

STIC

Please do a commercial and interference sequence search on SEQ ID NO:16 and 27 of this application.

Please provide a paper copy of all results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

RECEIVED
SEP 15 2005
STIC-BIOTECH/CHEM. DIVISION
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 9/16/05
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search: _____
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

THIS PAGE BLANK (USPTO)


```

RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
DR J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61554; CAA43752.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1 Potential.
FT SIGNAL <1 22 type A exotoxin.
FT CHAIN 23 >220
FT NON_TER 220 220
SQ SEQUENCE 220 AA; 25600 MW; 92DB096E57906DF6 CRC64;

Query Match 41.1%; Score 1027.5; DB 2; Length 220;
Best Local Similarity 98.0%; Pred. No. 1.4e-58;
Matches 194; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 23 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82

QY 62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIKKIVVK 120
Db 83 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLIPIKKIVVK 142

QY 121 VSIDGIQSLSPDIETNKKMVTQAQLDYKVRKYLTDNKLTYNGPSKYETGYIKFIPKNKE 180
Db 143 VSIDGIQSLSPDIETNKKMVTQAQLDYKVRKYLTDNKLTYNGPSKYETGYIKFIPKNKE 202

QY 181 SFWDFPFPEPEFTQSKYL 198
Db 203 SFWDFPFPEPEFTQSKYL 220

RESULT 12
ID Q54696 PRELIMINARY; PRT; 236 AA.
AC Q54696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
DR J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61573; CAA43771.1; -.
DR FIR; S18789; S18789.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.

```

```

DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1 Potential.
FT SIGNAL <1 22 type A exotoxin.
FT CHAIN 23 >236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 39.5%; Score 986.5; DB 2; Length 236;
Best Local Similarity 88.2%; Pred. No. 6.9e-56;
Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 2 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 23 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82

QY 62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIKKIVVK 120
Db 83 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLIPIKKIVVK 142

QY 121 VSIDGIQSLSPDIETNKKMVTQAQLDYKVRKYLTDNKLTYNGPSKYETGYIKFIPKNKE 180
Db 143 VSIDGIQSLSPDIETNKKMVTQAQLDYKVRKYLTDNKLTYNGPSKYETGYIKFIPKNKE 202

QY 181 SFWDFPFPEPEFTQSKYLMIYKDNETLDSNT 211
Db 203 TFWDFPFPEPEFTQSKYLMIYKDNETLDSNT 233

RESULT 13
QY38P4 PRELIMINARY; PRT; 222 AA.
ID Q938P4;
AC Q938P4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22508029; PubMed=12620634;
RA Kalia A., Bessen D.E.;
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT isolates of group G streptococci.";
DR FEMS Microbiol. Lett. 219:291-295 (2003).
DR EMBL; AY049745; AAL06068.1; -.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1

```


RESULT 7

Q54779 PRELIMINARY; PRT; 236 AA.
 ID AC Q54779; Q54736; Q54740; Q54741;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Type A exotoxin precursor (Fragment).
 GN Name=speA;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS485, MGAS158, MGAS491, MGAS495, and MGAS624;
 RX MEDLINE=92044323; PubMed=1940804;
 RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RT "Characterization and clonal distribution of four alleles of the speA
 gene encoding pyogenic exotoxin A (scarlet fever toxin) in
 RT Streptococcus pyogenes.";
 RL J. Exp. Med. 174:1271-1274 (1991).
 DR EMBL; X61569; CAA43767.1; -;
 DR EMBL; X61568; CAA43766.1; -;
 DR EMBL; X61570; CAA43768.1; -;
 DR EMBL; X61571; CAA43769.1; -;
 DR EMBL; X61572; CAA43770.1; -;
 DR PIR; A60108; A60108.
 DR HSSP; P01552; 1SEB.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_toxin_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT NON_TER 1 1 Potential.
 FT SIGNAL <1 22 type A exotoxin.
 FT CHAIN 23 >236
 FT NON_TER 236 236
 SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 43.9%; Score 1096.5; DB 2; Length 236;
 Best Local Similarity 98.6%; Pred. No. 5.5e-63;
 Matches 208; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 2 QQDPDPSQLHRSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
 DB 23 QQDPDPSQLHRSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82
 QY 62 ELKNQEMATLFDKKNIDYGVYHLYCYLCENASACI-GGVTNREGNHLIPIPKIVVK 120
 DB 83 ELKNQEMATLFDKKNIDYGVYHLYCYLCENASACIYGGVTNHEGNHLIPIPKIVVK 142
 QY 121 VSIDGIQSLSFDIETNKKMVAQELDYKVKYLTNDKQLYTNGPSKYETGIKFIPIKNKE 180
 DB 143 VSIDGIQSLSFDIETNKKMVAQELDYKVKYLTNDKQLYTNGPSKYETGIKFIPIKNKE 202
 QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNT 211
 DB 203 SFWDFPFPEFTQSKYLMYKDNETLDSNT 233

RESULT 8

Q9R931 PRELIMINARY; PRT; 222 AA.
 ID AC Q9R931; Q9R931;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Exotoxin A (Fragment).
 GN Name=speA;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D709;
 RX MEDLINE=99137798; PubMed=99523369;
 RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
 RT Hollingshead S.K., Beall B.;
 RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
 tropism in group A streptococci.";
 RL Infect. Dis. 179:627-636(1999).
 DR EMBL; AF055698; AAD11624.1; -;
 DR PIR; A60108; A60108.
 DR HSSP; P01552; 1SEB.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_toxin_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 222 222
 SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 43.8%; Score 1095.5; DB 2; Length 222;
 Best Local Similarity 98.1%; Pred. No. 5.9e-63;
 Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
 QY 2 QQDPDPSQLHRSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
 DB 11 QQDPDPSQLHRSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 70
 QY 62 ELKNQEMATLFDKKNIDYGVYHLYCYLCENASACI-GGVTNREGNHLIPIPKIVVK 120
 DB 71 ELKNQEMATLFDKKNIDYGVYHLYCYLCENASACIYGGVTNHEGNHLIPIPKIVVK 130
 QY 121 VSIDGIQSLSFDIETNKKMVAQELDYKVKYLTNDKQLYTNGPSKYETGIKFIPIKNKE 180
 DB 131 VSIDGIQSLSFDIETNKKMVAQELDYKVKYLTNDKQLYTNGPSKYETGIKFIPIKNKE 190
 QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNT 211
 DB 191 SFWDFPFPEFTQSKYLMYKDNETLDSNT 221

RESULT 9

Q9R931 PRELIMINARY; PRT; 236 AA.
 ID AC Q9R931; Q9R931;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Type A exotoxin precursor (Fragment).
 GN Name=speA;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;

```

RESULT 6
SPEA_STRPY
ID _SPEA_STRPY STANDARD; PRT; 251 AA.
AC P62560; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_taxid=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12."
RL Infect. Immun. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italien J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT receptors."
RL EMBO J. 18:9-21(1999).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U40453; AAC48868.1; -.
CC EMBL; X01929; CAA27568.1; -.
CC PIR; A26152; A26152.
CC PDB; 1B12; X-ray; -.
CC PDB; 1FNU; X-ray; -.
CC PDB; 1FNU; X-ray; -.
CC PDB; 1FNW; X-ray; -.
CC PDB; 1HA5; X-ray; -.
CC PDB; 1HA5; X-ray; -.
CC PDB; 1LOX; X-ray; -.
CC InterPro; IPR008992; Bact_endotox.
CC InterPro; IPR006177; Bctrl_tox.
CC InterPro; IPR006123; Stap/Strep_toxin.
CC InterPro; IPR006126; Staph/Strep_tox.
CC InterPro; IPR006173; Staph_tox_08.
CC Pfam; PF02876; Stap_Strp_tox_C; 1.

```

```

DR PF01123; Stap_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Signal; Toxin.
FT SIGNAL 1 30 Exotoxin type A.
FT CHAIN 31 251
FT DISULFID 117 128
FT CONFLICT 6 6
FT CONFLICT 17 18 K -> E (in Ref. 2).
FT CONFLICT 25 35 VT -> MK (in Ref. 2).
FT CONFLICT 40 40 SOEVFAQDDPD -> LPKGICSTRPK (in Ref. 2).
FT CONFLICT 43 43 H -> Q (in Ref. 2).
FT CONFLICT 47 59 S -> N (in Ref. 2).
FT CONFLICT 129 129 NLQNIYFLYEGDP -> TPKIYIFPMRVTL (in Ref.
FT CONFLICT 129 129 I -> L (in Ref. 2).
FT CONFLICT 165 178 TNKKWVTAQELDYK -> QIKNGNCSRIQSVT (in Ref.
FT TURN 36 38
FT HELIX 42 44
FT TURN 46 48
FT HELIX 49 56
FT STRAND 60 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT STRAND 82 82
FT TURN 83 84
FT STRAND 85 85
FT STRAND 87 91
FT HELIX 95 102
FT TURN 103 103
FT STRAND 106 110
FT STRAND 113 113
FT TURN 115 116
FT TURN 121 122
FT STRAND 126 130
FT STRAND 133 135
FT TURN 137 138
FT STRAND 140 153
FT TURN 154 155
FT STRAND 156 167
FT STRAND 169 171
FT HELIX 172 186
FT STRAND 197 205
FT STRAND 212 215
FT HELIX 224 227
FT STRAND 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 251
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCCBFC3 CRC64;
Query Match 45.2%; Score 1129; DB 1; Length 251;
Best Local Similarity 97.7%; Pred. No. 4.7e-65;
Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;
QY 2 QODPPSQLRHSSLVKNLQNIYFLYEGDPVTHENVKSVVDQLRSHDLIYNVSGPNYDKLKT 61
DB 31 QODPPSQLRHSSLVKNLQNIYFLYEGDPVTHENVKSVVDQLRSHDLIYNVSGPNYDKLKT 90
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI -GGVTNREGNHLIPIKKIVVK 120
DB 91 ELKQEMATLFDKKNVDYGVVEYHLCYLCEAERSACI -GGVTNREGNHLIPIKKIVVK 150
QY 121 VSIDGIQSLSPDIETNKKQWVTAQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKNKE 180
DB 151 VSIDGIQSLSPDIETNKKQWVTAQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKNKE 210
QY 181 SFWDFPFPEPEFTQSKYLMYKDNFTLDSNT -QIEVILTTK 220
DB 211 SFWDFPFPEPEFTQSKYLMYKDNFTLDSNTSQIEVILTTK 251

```

```

OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MGAS315 / Serotype M3;
RC MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=SSI-1;
RC MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055 (2003).
DR EMBL; AF014161; AAM79908.1; -.
DR EMBL; AP005142; BAC63655.1; -.
DR PIR; A60108; A60108.
DR HSP; P01552; LSEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_cox.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;

Query Match 45.2%; Score 1130; DB 2; Length 251;
Best Local Similarity 98.2%; Pred. No. 4.1e-65;
Matches 217; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 2 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
DB 31 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90

QY 62 ELKQEMATLFDKKNIDYGVYHLYCYLCENASACI-GGVNREGNHLIIPKKIVVK 120
DB 91 ELKQEMATLFDKKNIDYGVYHLYCYLCENASACIYGGVTHNEGNHLIIPKKIVVK 150

QY 121 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTNKNQLYTNGPSKYETGYIKFIPKKE 180
DB 151 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTNKNQLYTNGPSKYETGYIKFIPKKE 210

QY 181 SFWDFPPEPFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
DB 211 SFWDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 5
ID SPFA_STRP8 STANDARD; PRT; 251 AA.
AC P62561; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)

```

```

DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA; OrderedLocuaNames=speyM18_0393;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN SEQUENCE FROM N.A.
RP STRAIN=MGAS8232 / Serotype M18;
RC PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic fever
CC (By similarity).
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain (By similarity).
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE009982; AAL37141.1; -.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_cox.
DR Pfam; PF02876; Staph_stp_toxin; 1.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome; Signal; Toxin.
KW SIGNAL 1 30 By similarity.
FT CHAIN 31 251 Exotoxin type A.
FT DISULFD 117 128 By similarity.
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCCBCFCC3 CRC64;

Query Match 45.2%; Score 1129; DB 1; Length 251;
Best Local Similarity 97.7%; Pred. No. 4.7e-65;
Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 2 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
DB 31 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90

QY 62 ELKQEMATLFDKKNIDYGVYHLYCYLCENASACI-GGVNREGNHLIIPKKIVVK 120
DB 91 ELKQEMATLFDKKNIDYGVYHLYCYLCENASACIYGGVTHNEGNHLIIPKKIVVK 150

QY 121 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTNKNQLYTNGPSKYETGYIKFIPKKE 180
DB 151 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTNKNQLYTNGPSKYETGYIKFIPKKE 210

QY 181 SFWDFPPEPFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
DB 211 SFWDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

```


RL Microb. Pathog. 15:327-346(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A-20 / Serotype M1,T1;
RA Wu J.-J.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=SV / Serotype M23;
RA Hong K.;
RL "A novel cloning method used arbitrarily primed PCR.";
RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.07159398;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Berses S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okanashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution";
RL Genome Res. 13:1042-1055(2003).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Rickiells S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RN [9]
RP PRELIMINARY SEQUENCE OF 28-86 AND 121-398.
RA Yonaha K., Elliott S.D., Liu T.-Y.;
RT "Primary structure of zymogen of streptococcal proteinase.";
RL J. Protein Chem. 1:317-334(1982).
RN [10]
RP PRELIMINARY SEQUENCE OF 146-398.
RX MEDLINE=76190087; PubMed=1270417;
RA Tai J.-Y., Kortt A.A., Liu T.-Y., Elliott S.D.;
RT "Primary structure of streptococcal proteinase. III. Isolation of
RT cyanogen bromide peptides: complete covalent structure of the
RT polypeptide chain.";
RL J. Biol. Chem. 251:1955-1959(1976).
RN [11]
RP FUNCTION.
RC STRAIN=NZ131 / Serotype M49,T14;
RX MEDLINE=99081733; PubMed=9864206;
RA Kuo C.-F., Wu J.-J., Tsai P.-J., Kao F.-J., Lei H.-Y., Lin M.T.,
RA Lin Y.-S.;
RT "Streptococcal pyrogenic exotoxin B induces apoptosis and reduces
RT phagocytic activity in U937 cells.";
RL Infect. Immun. 67:126-130(1999).
RN [12]
RP FUNCTION.
RC STRAIN=A-20 / Serotype M1,T1;
RX MEDLINE=99386817; PubMed=10456871;
RA Tsai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;
RT "Group A Streptococcus induces apoptosis in human epithelial cells.";
RL Infect. Immun. 67:4334-4339(1999).
RN [13]
RP FUNCTION.
CC -!- FUNCTION: Important streptococcal virulence factor which cleaves
CC human fibronectin and degrades vitronectin. Also cleaves human
CC IL1B precursor to form biologically active IL1B. Can induce
CC apoptosis in human monocytes and epithelial cells in vitro, and
CC reduces phagocytic activity in monocytic cells. Thus, may play a
CC role in bacterial colonization, invasion, and inhibition of wound
CC healing.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage with hydrophobic
CC residues at P2, P1 and P1'.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the peptidase C10 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M86905; AAA26978.1; -
DR EMBL; L26125; AAA26979.1; -
DR EMBL; L26126; AAA26992.1; -
DR EMBL; L26127; AAA26993.1; -
DR EMBL; L26128; AAA26994.1; -
DR EMBL; L26130; AAA26996.1; -
DR EMBL; L26131; AAA26997.1; -
DR EMBL; L26132; AAA26998.1; -
DR EMBL; L26133; AAA26999.1; -
DR EMBL; L26134; AAA27000.1; -
DR EMBL; L26135; AAA27001.1; -
DR EMBL; L26136; AAA27002.1; -
DR EMBL; L26137; AAA27003.1; -
DR EMBL; L26138; AAA27004.1; -
DR EMBL; L26139; AAA27005.1; -
DR EMBL; L26140; AAA27006.1; -
DR EMBL; L26141; AAA27007.1; -
DR EMBL; L26142; AAA27008.1; -
DR EMBL; L26143; AAA27009.1; -
DR EMBL; L26144; AAA27010.1; -
DR EMBL; L26145; AAA27011.1; -
DR EMBL; L26146; AAA27012.1; -
DR EMBL; L26147; AAA27013.1; -
DR EMBL; L26148; AAA27014.1; -
DR EMBL; L26149; AAA27015.1; -
DR EMBL; L26150; AAA27016.1; -
DR EMBL; L26151; AAA26980.1; -
DR EMBL; L26152; AAA26981.1; -
DR EMBL; L26153; AAA26982.1; -
DR EMBL; L26154; AAA26983.1; -
DR EMBL; L26155; AAA26984.1; -
DR EMBL; L26156; AAA26985.1; -
DR EMBL; L26157; AAA26986.1; -
DR EMBL; L26158; AAA26987.1; -
DR EMBL; L26159; AAA26988.1; -
DR EMBL; L26160; AAA26989.1; -
DR EMBL; L26161; AAA26990.1; -
DR EMBL; L26162; AAA26991.1; -
DR EMBL; AF104940; AAD17930.1; -
DR EMBL; AB030578; BAB16027.1; -

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:48:38 ; Search time 148.406 Seconds
(without alignments)
1614.846 Million cell updates/sec

Title: US-10-002-784A-27

Perfect score: 2500

Sequence: 1 MQQDPDPQLHRSSLVKNLQ.....ALGTGGAGGNGYQSAVVG 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1327.5	53.1	398	1 SPB STRPY	P00788 streptococ
2	1324.5	53.0	398	2 Q9AJD2	Q9ajd2 streptococ
3	1293.5	51.7	344	2 Q93LQ2	Q93lq2 streptococ
4	1130	45.2	251	2 Q8K6K5	Q8k6k5 streptococ
5	1129	45.2	251	1 SPBA STRP8	P62561 streptococ
6	1129	45.2	251	1 SPBA STRPY	P62560 streptococ
7	1096.5	43.9	236	2 Q54779	Q54779 streptococ
8	1095.5	43.8	222	2 Q9R931	Q9r931 streptococ
9	1095.5	43.8	236	2 P97163	P97163 streptococ
10	1089.5	43.6	236	2 Q57453	Q57453 streptococ
11	1027.5	41.1	220	2 Q79AQ0	Q79aq0 streptococ
12	986.5	39.5	236	2 Q54696	Q54696 streptococ
13	981.5	39.3	222	2 Q938P4	Q938p4 streptococ
14	981.5	39.3	222	2 Q9S5Z4	Q9s5z4 streptococ
15	541	21.6	266	1 ETXB STAAU	P01552 staphylococ
16	516	20.6	239	2 Q53678	Q53678 staphylococ
17	516	20.6	271	2 Q9F0L6	Q9f0l6 staphylococ
18	515	20.6	239	2 Q06532	Q06532 staphylococ
19	515	20.6	239	2 Q06533	Q06533 staphylococ
20	515	20.6	266	2 Q8NXJ6	Q8nxj6 staphylococ
21	513	20.5	239	2 Q05157	Q05157 staphylococ
22	513	20.5	239	2 Q06531	Q06531 staphylococ
23	513	20.5	266	1 ETC3 STAAH	P23313 staphylococ
24	510	20.4	239	2 Q06535	Q06535 staphylococ
25	510	20.4	239	2 Q6ST49	Q6st49 staphylococ
26	510	20.4	266	1 ETC2 STAAU	P34071 staphylococ
27	509	20.4	266	1 ETC1 STAAU	P01553 staphylococ
28	505	20.2	239	2 Q06534	Q06534 staphylococ
29	504	20.2	234	2 Q9R5X4	Q9r5x4 staphylococ
30	492.5	19.7	260	2 Q54971	Q54971 streptococ
31	487.5	19.5	260	2 Q54738	Q54738 streptococ

32	487.5	19.5	260	2	Q79X14	Q79x14 streptococ
33	487.5	19.5	260	2	Q54739	Q54739 streptococ
34	484	19.4	264	2	Q764P6	Q764p6 staphylococ
35	482	19.3	259	2	Q936G4	Q936g4 staphylococ
36	479	19.2	259	2	Q76LS8	Q76ls8 staphylococ
37	478.5	19.1	222	2	Q6XZE6	Q6xze6 staphylococ
38	475.5	19.0	222	2	Q6XZE7	Q6xze7 staphylococ
39	468	18.7	261	2	Q8XXM5	Q8xxm5 staphylococ
40	468	18.7	261	2	Q8YCN4	Q8ycn4 staphylococ
41	468	18.7	261	2	Q6GFN0	Q6gfn0 staphylococ
42	457	18.3	261	2	Q6XXM3	Q6xxm3 staphylococ
43	454	18.2	261	2	Q6XXM4	Q6xxm4 staphylococ
44	445.5	17.8	214	2	Q6XZE8	Q6xze8 staphylococ
45	444	17.8	233	2	Q8RR77	Q8rr77 staphylococ

ALIGNMENTS

RESULT 1

SPB STRPY STANDARD; PRT; 398 AA.
 AC P00788; P26296; Q54960; Q54961; Q54962; Q54963; Q54964; Q54965;
 AC Q54966; Q54967; Q54968; Q57024; Q57082; Q57202; Q57211; Q57212;
 AC Q9S680;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Streptopain precursor (BC 3.4.22.10) (Streptococcal cysteine
 DE proteinase) (Streptococcus peptidase A) (SPP) (Exotoxin type B) (SPE
 DE B).
 GN Name=speB;
 GN OrderedLocNames=SPY2039, SPYM3_1742, SPS1739, SPYM18_2099;
 OS Streptococcus pyogenes,
 OS Streptococcus pyogenes (serotype M3), and
 OS Streptococcus pyogenes (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314, 198466, 186103;
 RN [1]
 RC SEQUENCE FROM N.A., AND SEQUENCE OF 28-32 AND 146-162.
 RC STRAIN=86-858, and NY-5;
 RX MEDLINE=90330563; PubMed=2198264;
 RA Hauser A.R., Schlievert P.M.;
 RT "Nucleotide sequence of the streptococcal pyrogenic exotoxin type B
 RT gene and relationship between the toxin and the streptococcal
 RT proteinase precursor."
 RL J. Bacteriol. 172:4536-4542 (1990).
 RN [2]
 RC SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=1226 / Serotype M44, 1233 / Serotype M17, 1251 / Serotype M3,
 RC 1289 / Serotype M5, 1294 / Serotype M19, 156 / Serotype M18,
 RC 157 / Serotype M3, 1590, 162 / Serotype M22, 165 / Serotype M,
 RC 168 / Serotype M66, 1719 / Serotype T8, 1832 / Serotype M76,
 RC 1838 / Serotype M27, 1841 / Serotype M41, 1842 / Serotype M43,
 RC 1864 / Serotype M56, 1870, 1871, 1872, 1882 / Serotype M59, 1893,
 RC 1896 / Serotype M10, 1898 / Serotype M15, 1901 / Serotype M23,
 RC 1911 / Serotype M75, 1914A, 1990 / Serotype M, 1991 / Serotype M,
 RC 2017 / Serotype M, 2018 / Serotype M, 262 / Serotype M,
 RC 282 / Serotype M12, 289 / Serotype T28, 300 / Serotype M18,
 RC 302 / Serotype M73, 303 / Serotype M6, 315 / Serotype M3,
 RC 317 / Serotype M, 321 / Serotype M4, 327 / Serotype M2,
 RC 366 / Serotype M31, 427 / Serotype M31, 429 / Serotype M8,
 RC 587 / Serotype M28, 650 / Serotype M11, 659 / Serotype M13,
 RC 660 / Serotype M14, 684 / Serotype M24, 686 / Serotype M25,
 RC 719 / Serotype M49, 75 / Serotype M3, 758 / Serotype M75, and
 RC 789 / Serotype M1, 796 / Serotype M9, 800 / Serotype M9, and
 RC 807 / Serotype M33;
 RC MEDLINE=94285789; PubMed=7516997; DOI=10.1006/mpat.1993.1083;
 RX Kapur V., Topouzis S., Majesky M.W., Li L.L., Hamrick M.R.,
 RA Hamill R.J., Patti J.M., Musser J.M.;
 RT "A conserved Streptococcus pyogenes extracellular cysteine protease
 RT cleaves human fibronectin and degrades vitronectin.";

THIS PAGE BLANK (USPTO)

F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin B #status experimental <MAT>
F;120-140/Disulfide bonds: #status experimental

Query Match 21.6%; Score 541; DB 1; Length 266;
Best Local Similarity 47.7%; Pred. No. 6.3e-28;
Matches 113; Conservative 39; Mismatches 67; Indels 18; Gaps 7;

QY 2 QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGP---PNYD 57
Db 30 QPDPTDELHKSSEFTGTGNNKYLDDHYVSATKVSVDKFLAHLDIYNISDKKLKNYD 89

QY 58 KLKTELKNQEMATLFDKNIDYGVYHLCYLCE-----NAERSACIGGVNREGNH 110
Db 90 KVKTLLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITKHEGHN 149

QY 111 LEIP--KKIVKVSIDIGISLQSLFDIETNKKMVTAEQLDYKVRKYLTDNKLQLYTNGSPSKYE 168
Db 150 FDNGLQNLVRYENVKRNITISFEVQTDKKSVTAEQLDIKARNFLINKNLYEFNSSPYE 209

QY 169 TGYIKFIPKNKESFWDFPPEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 220
Db 210 TGYIKFIENNGNTFWIDMMPAPGDKFDQSKYLMYNDNKTVDKSKVKIEVHLTTK 264

RESULT 10
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60114; B60114; A33866
R;Bohach, G.A.; Schlievert, P.M.
Infected. Immun. 57, 2249-2252, 1999
A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins

F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin B #status experimental <MAT>
F;120-140/Disulfide bonds: #status experimental

Query Match 20.5%; Score 513; DB 2; Length 266;
Best Local Similarity 45.1%; Pred. No. 4.1e-26;
Matches 106; Conservative 43; Mismatches 70; Indels 16; Gaps 6;

QY 2 QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSG---PNYD 57
Db 30 QPDPTDELHKSSEFTGTGNNKYLDDHYVSATKVSVDKFLAHLDIYNISDKKLKNYD 89

QY 58 KLKTELKNQEMATLFDKNIDYGVYHLCYLCE-----NAERSACIGGVNREGNH 110
Db 90 KVKTLLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITKHEGHN 149

QY 111 LEIP--KKIVKVSIDIGISLQSLFDIETNKKMVTAEQLDYKVRKYLTDNKLQLYTNGSPSKYE 168
Db 150 FDNGLQNLVRYENVKRNITISFEVQTDKKSVTAEQLDIKARNFLINKNLYEFNSSPYE 209

QY 169 TGYIKFIPKNKESFWDFPPEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 220
Db 210 TGYIKFIENNGNTFWIDMMPAPGDKFDQSKYLMYNDNKTVDKSKVKIEVHLTTK 264

RESULT 11
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: S06356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness

A;Reference number: A60114; MUID:89277549; PMID:2543637
A;Accession: A60114
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P34071
A;Accession: B60114
A;Molecule type: protein
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests t
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:gl53003; PIDN:AAA26624.1; PID:gl53004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 20.4%; Score 510; DB 2; Length 266;
Best Local Similarity 44.3%; Pred. No. 6.4e-26;
Matches 104; Conservative 45; Mismatches 70; Indels 16; Gaps 6;

QY 2 QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSG---PNYD 57
Db 30 QPDPTDELHKSSEFTGTGNNKYLDDHYVSATKVSVDKFLAHLDIYNISDKKLKNYD 89

QY 58 KLKTELKNQEMATLFDKNIDYGVYHLCYLCE-----NAERSACIGGVNREGNH 110
Db 90 KVKTLLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITKHEGHN 149

QY 111 LEIP--KKIVKVSIDIGISLQSLFDIETNKKMVTAEQLDYKVRKYLTDNKLQLYTNGSPSKYE 168
Db 150 FDNGLQNLVRYENVKRNITISFEVQTDKKSVTAEQLDIKARNFLINKNLYEFNSSPYE 209

QY 169 TGYIKFIPKNKESFWDFPPEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 220
Db 210 TGYIKFIENNGNTFWIDMMPAPGDKFDQSKYLMYNDNKTVDKSKVKIEVHLTTK 264

RESULT 11
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: S06356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness
A;Reference number: S06356; MUID:88038352; PMID:2823067
A;Accession: S06356
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P01553; EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
R;Schmidt, J.J.; Spers, L.
J. Biol. Chem. 258, 6300-6306, 1983
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A;Reference number: A01816; MUID:83213327; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C;Genetics:
A;Gene: entC1
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
F;120-137/Disulfide bonds: #status experimental

QY 62 ELKQEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIEIPKKIIVVK 120
DB 83 ELKQEMATLFDKKNVDIIVSVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIIVVK 142
QY 121 VSDIGQSLSFDIETNKKMWTQAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
DB 143 VSDIGQSLSFDIETNKKMWTQAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 202
QY 181 SFWDFPPEFTQSKYLMYKDNETLDSNT 211
DB 203 SFWDFPPEFTQSKYLMYKDNETLDSNT 233
RESULT 6
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate California
N;Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEL>
A:Cross-references: UNIPROT:Q54696; EMBL:X61573; NID:g47303; PIDN:CAA43771.1; PID:g47304
A:Note: the nucleotide sequence was submitted to the EMBL data library, September 1991
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>
Query Match 39.5%; Score 986.5; DB 2; Length 236;
Best Local Similarity 88.2%; Pred. No. 6.9e-57;
Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
QY 2 QDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 61
DB 23 QDDPNSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGNLNVDKLT 82
QY 62 ELKQEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIEIPKKIIVVK 120
DB 83 ELKQEMATLFDKKNVDIIVSVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKNILVK 142
QY 121 VSDIGQSLSFDIETNKKMWTQAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
DB 143 VSDIGQSLSFDIETSKKMWTQAQELDYKVRKHLTDNKKQLYTNGPSKYETGYIKFISQKE 202
QY 181 SFWDFPPEFTQSKYLMYKDNETLDSNT 211
DB 203 TFWDFPPEFTQSKYLMYKDNETLDSNT 233
RESULT 7
A26152
Streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N;Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26152
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA

A:Residues: 1-250 <JOH>
A:Cross-references: UNIPROT:P08095
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 37.5%; Score 938.5; DB 1; Length 250;
Best Local Similarity 84.9%; Pred. No. 9.8e-54;
Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;

QY 5 PDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 64
DB 34 PKPSQLQRSNLVKTFKIYIFFMRVTLVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 93

QY 65 NOEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIEIPKKIIVVK 123
DB 94 NOEMATLFDKKNVDIIVSVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIIVVK 153

QY 124 DGIQSLSDIETNKKMWTQAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKESFW 183
DB 154 DGIQSLSDIETQIKY-GNCSRIISYTVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKESFW 212

QY 184 FDFPPEPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220

DB 213 FDFPPEPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 250

RESULT 8

ENSAB6

enterotoxin B precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004

A:Accession: S27360; A92065; S27240; A01815

R:Jones, C.L.; Khan, S.A.

J. Bacteriol. 166, 29-33, 1986

A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.

A:Reference number: S27360; MUID:86168029; PMID:3957869

A:Accession: S27360

A:Molecule type: DNA

A:Residues: 1-266 <JON>

A:Cross-references: UNIPROT:P01552; EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g1530

A:Experimental source: strain S6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3518-3525, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromid

A:Reference number: A92065; MUID:71007902; PMID:5470821

A:Accession: A92065

A:Molecule type: protein

A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',

A:Experimental source: strain S-6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3511-3517, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositi

A:Reference number: A92064; MUID:71007901; PMID:5470820

A:Contents: annotation; chymotryptic peptides

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3493-3510, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compositi

A:Reference number: A92063; MUID:71007900; PMID:5470819

A:Contents: annotation; tryptic peptides

R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.

Biochemistry 4, 1011-1016, 1965

A:Title: Purification of staphylococcal enterotoxin B.

A:Reference number: A90548; MUID:66035792; PMID:4953912

A:Contents: annotation: biological source of protein

R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni

Eur. J. Biochem. 209, 823-828, 1992

A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B

A:Reference number: S27240; MUID:93049338; PMID:1425690

A:Accession: S27240

A:Molecule type: protein

A:Residues: 28-42; 128-148 <ALA>

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin; extracellular protein; toxin

A;Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S18783; S18793; S18794; S18801; S18798
R;Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18783
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61568; NID:G47289; PIDN:CAA43766.1; PID:G47290
A;Experimental source: strain MGAS158 isolate Nebraska unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18793
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61569; NID:G47313; PIDN:CAA43767.1; PID:G47314
A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18794
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61570; NID:G47315; PIDN:CAA43768.1; PID:G47316
A;Experimental source: strain MGAS491 isolate United Kingdom unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18801
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61572; NID:G47333; PIDN:CAA43770.1; PID:G47334
A;Experimental source: strain MGAS624 isolate Germany unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18798
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61571; NID:G47323; PIDN:CAA43769.1; PID:G47324
A;Experimental source: strain MGAS495 isolate Germany unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA3
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 43.9%; Score 1096.5; DB 2; Length 236;
Best Local Similarity 98.6%; Pred. No. 5.1e-64;
Matches 208; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db |||||
23 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82

QY 62 ELKNQEMATLFDKNDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLIPIPKIVVK 120
Db |||||
83 ELKNQEMATLFDKNDIYGVVEYHLCYLCEAERSACIYGGVTHNEGNHLIPIPKIVVK 142

QY 121 VSIDGIQSLSFDIETNKKMWTAQLDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
Db |||||
143 VSIDGIQSLSFDIETNKKMWTAQLDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 202

QY 181 SFWDFEFPPEFTQSKYLMYKDNETLDSNT 211
Db |||||
203 SFWDFEFPPEFTQSKYLMYKDNETLDSNT 233

RESULT 5
S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phase (strain MGAS250 iso1

N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain
isolate United Kingdom; strain MGAS496 isolate Germany
C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R;Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18786
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61561; NID:G47297; PIDN:CAA43759.1; PID:G47298
A;Experimental source: strain MGAS250 isolate California unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18787
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61562; NID:G47299; PIDN:CAA43760.1; PID:G47300
A;Experimental source: strain MGAS251 isolate California unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18788
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61563; NID:G47301; PIDN:CAA43761.1; PID:G47302
A;Experimental source: strain MGAS256 isolate California unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18790
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61564; NID:G47305; PIDN:CAA43762.1; PID:G47306
A;Experimental source: strain MGAS285 isolate Colorado unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18792
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61565; NID:G47311; PIDN:CAA43763.1; PID:G47312
A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18795
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61566; NID:G47317; PIDN:CAA43764.1; PID:G47318
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18799
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NE>
A;Cross-references: EMBL:X61567; NID:G47325; PIDN:CAA43765.1; PID:G47326
A;Experimental source: strain MGAS496 isolate Germany unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA2
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 43.6%; Score 1089.5; DB 2; Length 236;
Best Local Similarity 97.6%; Pred. No. 1.5e-63;
Matches 206; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db |||||
23 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82

RESULT 5
S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phase (strain MGAS250 iso1

A>Title: Primary structure of zymogen of streptococcal proteinase.
A:Reference number: S07668
A:Accession: S07668
A:Molecule type: protein
A:Residues: 1-337 <YON>
R:Tai, J.Y.; Kortt, A.A.; Liu, T.Y.; Elliott, S.D.
J. Biol. Chem. 251, 1955-1959, 1976

J>Title: Primary structure of streptococcal proteinase. III. Isolation of cyanogen bromide fragments from Streptococcus pyogenes strain WCAS156 isolate Nebraska unassigned.

A:Reference number: A00978; MUID:76190087; PMID:1270417
A:Accession: A00978
A:Molecule type: protein
A:Residues: 85-107, 'L', 109-244, 'N', 246-337 <TAI>
A>Note: Trp-298 is at the binding site of the enzyme
C:Comment: This enzyme can remove the activation peptide from the proenzyme.
C:Superfamily: streptococcal cysteine proteinase
C:Keywords: cysteine proteinase; hydrolase; zymogen
F:1-84/Domain: activation peptide #status experimental <PRO>
F:85-337/Product: streptopain #status experimental <MAT>
F:131,279/Active site: Cys, His #status experimental

Query Match 47.9%; Score 1198; DB 1; Length 337;
Best Local Similarity 84.1%; Pred. No. 2.2e-70;
Matches 233; Conservative 14; Mismatches 20; Indels 10; Gaps 4;

Gy 197 YLMTYKNETLDNSTQTEVILTT---KPVVVKSLDSKGIIHYNOGNPNYNLLTPVIEKVCP 253
Db | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Gy 63 YVEIKENKKLDT-----TVAGTAEIKQPVVVKSLDSKGIIHYNOGNPNYNLLTPVIEKVCP 117
Db ||:||::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Gy 254 GEQSFGVAHATGCVCATATAQIMKYHNYPKNGLKDYYTLSSNNPYFNHPKNLPFAALSTR 313
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Gy 118 GEQSFGVAHTGHCVATATAQIMKYHNYPDKLGKNTYTYSNPDPDYFDHPKNLPFAALSTR 177
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Gy 314 QYNWNINLTPTSGRESNVQNKAISELMADVGISVDMDYGPPSSGSAGSRVRQRALKENFYGY 373
Db |:|:|:|:|:~ODWEAQIDKELSONQPVYIOG-KGVGGHAFFVIDDAGRNFYHVNWG 431
Gy 374 NQSVHQINRSDFS--ODWEAQIDKELSONQPVYIOG-KGVGGHAFFVIDDAGRNFYHVNWG 431
Db |:|:|:|:~QDWQAQIDKELSONQPVYIOG-KGVGGHAFFVIDDAGRNFYHVNWG 431
Gy 238 NQSVHQIQDRGFSDXQDWQAQIDKELSONQPVYIOG-KGVGGHAFFVIDDAGRNFYHVNWG 297
Db |:|:|:|:~QDWQAQIDKELSONQPVYIOG-KGVGGHAFFVIDDAGRNFYHVNWG 297
Gy 432 WGWVSDFGRDLNLPSALGTGGCGGPGNGVQSAVWG 468
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Gy 298 WGWVSDFGRDLNLPSALGTGGCGGPGNGVQSAVWG 334
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 3

S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N:Alternate names: erythrotoxic toxin; scarlet fever toxin
C:Species: Streptococcus pyogenes phage T12
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R:Weeks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986

A>Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrotoxic toxin)

A:Reference number: S29659; MUID:86166804; PMID:3514452
A:Accession: S29659
A:Molecule type: DNA
A:Residues: 1-251 <WEBE>
A:Cross-references: GB:U40453; EMBL:M19350; NID:g1877426; PID:AAC48868.1; PID:g1877430
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991

A>Title: Characterization and clonal distribution of four alleles of the speA gene encoded by Streptococcus pyogenes strains MGAS156 isolate Nebraska unassigned.

A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18782
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEL>
A:Cross-references: EMBL:X61560; NID:g47287; PID:CAA43758.1; PID:g47288
A:Experimental source: Streptococcus pyogenes strain WCAS156 isolate Nebraska unassigned
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18784
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 9-244 <NEA>
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
A:Experimental source: Streptococcus pyogenes strain MGA5165 isolate Minnesota unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18785
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE2>
A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294
A:Experimental source: Streptococcus pyogenes strain MGA5167 isolate Texas unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18791
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE3>
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310
A:Experimental source: Streptococcus pyogenes strain MGA5327 isolate Arizona unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18796
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEO>
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320
A:Experimental source: Streptococcus pyogenes strain MGA5493 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18797
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEH>
A:Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
A:Experimental source: Streptococcus pyogenes strain MGA5494 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18800
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-228 <NES>
A:Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328
A:Experimental source: Streptococcus pyogenes strain MGA5500 isolate New Zealand unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA; speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-30/Domain: signal
F:31-251/Product: exotoxin type A #status predicted <SIG>
Query Match 45.2%; Score 1129; DB 1; Length 251;
Best Local Similarity 97.7%; Pred. No. 4.4e-66;
Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;
Qy 2 QQDPPSQHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNVDKLT 61
Db 31 QQDPPSQHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNVDKLT 90
Qy 62 ELKQEMATLFDKNDIYGVYYHLCYLCENASACI-GGVTNREGNHLLEIPKKIVVK 120
Db 91 ELKQEMATLFDKNDIYGVYYHLCYLCENASACIYGGVTNHEGNHLLEIPKKIVVK 150
Qy 121 VSIDGIQSLSPDIETNKKMVTQAQLDYKVRKYLTDNKQLYTNGPSKYETGYIKPIPKNK 180
Db 151 VSIDGIQSLSPDIETNKKMVTQAQLDYKVRKYLTDNKQLYTNGPSKYETGYIKPIPKNK 210
Qy 181 SFWDFDFPEPFTQSKYLMYIKDNETLDSNT-QIEVYLLTK 220
Db 211 SFWDFDFPEPFTQSKYLMYIKDNETLDSNTS-QIEVYLLTK 251
RESULT 4
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGA5158 isolate)
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 17, 2005, 01:00:14 ; Search time 33.847 Seconds
(without alignments)
1330.382 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDPDPQLHRSSLVKNLQ.....ALGTGGAGGFGNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pir1:.*
2: Pir2:.*
3: Pir3:.*
4: Pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	ID	Description	
1	1327.5	53.1	398 2 A37768	streptococcal pyro	
2	1198	47.9	337 1 BPSOP	streptopain (EC 3.	
3	1129	45.2	251 1 S29659	exotoxin type A pr	
4	1096.5	43.9	236 2 S18783	exotoxin type A pr	
5	1089.5	43.6	236 2 S18786	exotoxin type A pr	
6	986.5	39.5	236 2 S18789	exotoxin A precurs	
7	938.5	37.5	250 1 A26152	streptococcal pyro	
8	541	21.6	266 1 ENSAB6	enterotoxin B prec	
9	513	20.5	266 2 S11885	enterotoxin C3 - S	
10	510	20.4	266 2 A60114	enterotoxin C-2 pr	
11	509	20.4	266 1 ENSAC1	enterotoxin C-1 pr	
12	444	17.8	258 2 G89968	extracellular ente	
13	422	16.9	886 2 T10890	cysteine proteinas	
14	303.5	12.1	136 2 A89969	enterotoxin YENT2	
15	295.5	11.8	258 2 A33953	enterotoxin D prec	
16	291.5	11.7	260 2 E89969	enterotoxin SeO (i	
17	279.5	11.2	260 2 C89984	enterotoxin P (imp	
18	263	10.5	240 2 G89991	extracellular ente	
19	262.5	10.5	258 2 H89968	enterotoxin SeN (i	
20	257.5	10.3	257 2 A28664	enterotoxin A prec	
21	256.5	10.3	257 2 A28179	enterotoxin B prec	
22	237.5	9.5	239 2 D89969	enterotoxin SEM (i	
23	218	8.7	242 2 C89969	extracellular ente	
24	183	7.3	235 2 A30509	exotoxin C precurs	
25	173	6.9	133 2 B89969	enterotoxin Vent1	
26	154.5	6.2	825 2 H82885	hypothetical prote	
27	137	5.5	2500 2 G71609	hypothetical prote	
28	132.5	5.3	231 2 D89807	exotoxin 11 (impor	
29	124.5	5.0	750 2 G81361	probable flagellin	

30	124.5	5.0	1183	2	F90559	conserved hypothet
31	123.5	4.9	616	2	G82885	hypothetical prote
32	123	4.9	227	2	C89808	exotoxin 15 (impor
33	123	4.9	1215	2	B48281	cytotoxin-associat
34	122.5	4.9	960	2	S72284	DNA-directed RNA p
35	122.5	4.9	1146	2	A89922	conserved hypothet
36	121	4.8	1881	2	H95076	zinc metalloprotei
37	120.5	4.8	378	2	AD1541	hypothetical prote
38	120.5	4.8	2401	2	T28676	rhostry protein -
39	119	4.8	351	2	D89991	hypothetical prote
40	118	4.7	1306	2	T28313	ORF MSV152 probabl
41	117	4.7	675	2	S16624	penicillin-binding
42	117	4.7	1186	2	C64588	cag pathogenicity
43	116.5	4.7	770	2	B48910	desmocollin 1a pre
44	116.5	4.7	824	2	A48910	desmocollin 1a pre
45	116.5	4.7	840	2	I37281	Dscia precursor -

ALIGNMENTS

RESULT 1

A37768
streptococcal pyrogenic exotoxin type B precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 22-Jun-1999
C:Accession: A37768
R:Hauser, A.R.; Schlievert, P.M.
J. Bacteriol. 172, 4536-4542, 1990
A:Title: Nucleotide sequence of the streptococcal pyrogenic exotoxin type B gene and re
A:Reference number: A37768; MUID:90330563; PMID:2198264
A:Accession: A37768
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-398 <HAU>
A:Cross-references: GB:M86905; GB:M35110; NID:g153818; PIDN:AAA26978.1; PID:g153819
C:Superfamily: streptococcal cysteine proteinase
C:Keywords: exotoxin

Query Match 53.1%; Score 1327.5; DB 2; Length 398;
Best Local Similarity 91.5%; Pred. No. 1.1e-78;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY	192	FTQSKYLMYKDNETHLSNTQIEVYLT---	KQPVVKSLDSDSGIHYNQGNPNLLTPVI	248
Db	120	FMES-YVQIKENKKLDT-----TYAGTABI	KQPVVKSLDSDSGIHYNQGNPNLLTPVI	173
QY	249	EKVKGEGSFGVQHAATGCVATATAQIMKYHNP	PNKGLDYTYTLSSNNPYNFHPKNLFA	308
Db	174	EKVKGEGSFGVQHAATGCVATATAQIMKYHNP	PNKGLDYTYTLSSNNPYNFHPKNLFA	233
QY	309	AISTQYNNNLLPTYSGRESNVQKMAISELMDV	IGISVDMYGPSSGAGSSRVQALK	368
Db	234	AISTQYNNNLLPTYSGRESNVQKMAISELMDV	IGISVDMYGPSSGAGSSRVQALK	293
QY	369	ENFGYNQVHQINRSDFS-QDWEAQIDKELSONQ	PVYQGGVKGHAFVIDGADGRNFI	426
Db	294	ENFGYNQVHQINRSDFSQDWEAQIDKELSONQ	PVYQGGVKGHAFVIDGADGRNFI	353
QY	427	HVNWGWGVSDGFFRLDALNPSALGTGGAGG	FNGYQSAVVG	468
Db	354	HVNWGWGVSDGFFRLDALNPSALGTGGAGG	FNGYQSAVVG	395

RESULT 2

BPSOP
streptopain (EC 3.4.22.10) precursor - Streptococcus pyogenes
N:Alternate names: streptococcal cysteine proteinase; streptococcal peptidase A
C:Species: Streptococcus pyogenes
C>Date: 24-Apr-1984 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C:Accession: S07668; A00978
R:Yonaha, K.; Elliott, S.D.; Liu, T.Y.
J. Protein Chem. 1, 317-334, 1982

THIS PAGE BLANK (USPTO)


```
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/767,687
;   FILING DATE: 29-Jan-2004
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/882,431B
;   FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Charles H. Harris
;   REGISTRATION NUMBER: 34,616
;   REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 619-2065
;   TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 251
;     TYPE: Amino Acid
;     STRANDEDNESS: Unknown
;     TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

Query Match          45.4%; Score 1136; DB 17; Length 251;
Best Local Similarity 98.2%; Pred. No. 1.1e-76;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY  2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
Db  31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90
QY  62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIVVK 120
Db  91 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150
QY  121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db  151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
QY  181 SFWDFPFPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db  211 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 13
US-10-428-817A-163
; Sequence 163, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 163
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-163

Query Match          45.2%; Score 1129; DB 16; Length 251;
Best Local Similarity 97.7%; Pred. No. 3.7e-76;
Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY  2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
Db  31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90
QY  62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIVVK 120
Db  91 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150
QY  121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db  151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
QY  181 SFWDFPFPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db  211 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 14
US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

Query Match          44.9%; Score 1122; DB 8; Length 251;
Best Local Similarity 97.3%; Pred. No. 1.2e-75;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY  2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
Db  31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90
QY  62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIVVK 120
Db  91 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150
QY  121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db  151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
QY  181 SFWDFPFPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db  211 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251
```

QY 61 TELKNQEMATLFDKKNIDYGVYYHLCYLCENAESACIYGGVTNREGNHLRIPKKIVVK 120
Db 61 TELKNQEMATLFDKKNIDYGVYYHLCYLCENAESACIYGGVTNREGNHLRIPKKIVVK 120
QY 121 VSIDGIQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGIQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWFDFPPEPTQSKYLMYKDNETLDSNTQIEVYLTTK 220
Db 181 SFWFDFPPEPTQSKYLMYKDNETLDSNTQIEVYLTTK 220

RESULT 10
US-08-882-431-16
; Sequence 16, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match 45.4%; Score 1136; DB 8; Length 251;
Best Local Similarity 98.2%; Pred. No. 1.1e-76;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;
QY 2 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 31 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90
QY 62 ELKNQEMATLFDKKNIDYGVYYHLCYLCENAESACI -GGVTNREGNHLRIPKKIVVK 120
Db 91 ELKNQEMATLFDKKNVDIYGVYYHLCYLCENAESACIYGGVTNREGNHLRIPKKIVVK 150
QY 121 VSIDGIQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180

Db 151 VSIDGIQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
QY 181 SFWFDFPPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db 211 SFWFDFPPEPTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 11
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US26030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16
Query Match 45.4%; Score 1136; DB 14; Length 251;
Best Local Similarity 98.2%; Pred. No. 1.1e-76;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;
QY 1 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 31 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90
QY 62 ELKNQEMATLFDKKNIDYGVYYHLCYLCENAESACI -GGVTNREGNHLRIPKKIVVK 120
Db 91 ELKNQEMATLFDKKNVDIYGVYYHLCYLCENAESACIYGGVTNREGNHLRIPKKIVVK 150
QY 121 VSIDGIQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 151 VSIDGIQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
QY 181 SFWFDFPPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db 211 SFWFDFPPEPTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 12
US-10-767-687-16
; Sequence 16, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh

```
RESULT 7
US-10-872-197A-25
; Sequence 25, Application US/10872197A
; Publication No. US20050059126A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOTSMIEIER
; APPLICANT: Ulrich KETTLING
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000203
; CURRENT APPLICATION NUMBER: US/10/872,197A
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-872-197A-25

Query Match          52.7%; Score 1316.5; DB 17; Length 371;
Best Local Similarity 91.1%; Pred. No. 6e-90;
Matches 257; Conservative 4; Mismatches 10; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGHIHQGNPNYLLTPVI 248
Db 93 FMES-YVEQIKENKKLDS-----TYAGTAEIKQPVVKSLLDSKGHIHQGNPNYLLTPVI 146
QY 249 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 308
Db 147 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 206
QY 309 AISTQYNNNNILPTYSGRESNVQKMAISELMADYGISVDMYDGPSSGAGSSRVQRAK 368
Db 207 AISTQYNNNNILPTYSGRESNVQKMAISELMADYGISVDMYDGPSSGAGSSRVQRAK 266
QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQG-GKVGGHAFVIDGADGRNPFY 426
Db 267 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQG-GKVGGHAFVIDGADGRNPFY 326
QY 427 HYNWGWGVSDDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
Db 327 HYNWGWGVSDDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 368

RESULT 8
US-11-021-951-25
; Sequence 25, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMIEIER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11

Query Match          46.7%; Score 1168; DB 14; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.7e-79;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQDPPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLK 60
Db 1 MQQDPPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLK 60
```


121 VSIDGQSLEFIDETNKKWMTAQELDYKVRKYLTONKOLYTNNGSPSKYETGYIKFIPKNKE 180
121 VSIDGQSLEFIDETNKKWMTAQELDYKVRKYLTONKQLYTNNGSPSKYETGYIKFIPKNKE 180
181 SFWDFPFPEFTQSKYLMYKDNETLDSNTQIEVLTQKQPVVKSLLDSKGIHYNQGNP 240
181 SFWDFPFPEFTQSKYLMYKDNETLDSNTQIEVLTQKQPVVKSLLDSKGIHYNQGNP 240
241 YNLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
241 YNLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
301 NHPKNLFAAISTROYNNILPTYSGRESNVQMAISELMADVGVSDMDYGPSSGSGS 360
301 NHPKNLFAAISTROYNNILPTYSGRESNVQMAISELMADVGVSDMDYGPSSGSGS 360
361 SRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSONQPVYQGVGGHAFVIGCA 420
361 SRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSONQPVYQGVGGHAFVIGCA 420
421 DGRNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
421 DGRNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468

RESULT 2
US-10-002-784A-25
; Sequence 25, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 25
; TYPE: PRT
; LENGTH: 248
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-B
US-10-002-784A-25

Query Match 53.3%; Score 1332; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.4e-91;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 221 QPVVKSLLDSKGIHYNQGNPNLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYH 280
Db 1 QPVVKSLLDSKGIHYNQGNPNLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYH 60
QY 281 YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTROYNNILPTYSGRESNVQMAISELM 340
Db 61 YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTROYNNILPTYSGRESNVQMAISELM 120
QY 341 ADVGISVDMYDGPSSGSGSSRRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSON 400
Db 121 ADVGISVDMYDGPSSGSGSSRRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSON 180
QY 401 QPVYQGVGGHAFVIGDAGGFNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFN 460
Db 181 QPVYQGVGGHAFVIGDAGGFNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFN 240
QY 461 GYQSAVVG 468
Db 241 GYQSAVVG 248

RESULT 3
US-10-428-817A-164
; Sequence 164, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164
; TYPE: PRT
; LENGTH: 398
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-164

Query Match 53.1%; Score 1327.5; DB 16; Length 398;
Best Local Similarity 91.5%; Pred. No. 1e-90;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIHYNQGNPNLLTPVI 248
Db 120 FMES-YVEQIKENKKLDT-----TYAGTAETKQPVVKSLLDSKGIHYNQGNPNLLTPVI 173
QY 249 EKVPGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLPA 308
Db 174 EKVPGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLPA 233
QY 309 AISTROYNNILPTYSGRESNVQMAISELMADVGVSDMDYGPSSGSGSSRRVQRALK 368
Db 234 AISTROYNNILPTYSGRESNVQMAISELMADVGVSDMDYGPSSGSGSSRRVQRALK 293
QY 369 ENFGYNQSVHQNRSDFS-QDWEAQIDKELSONQPVYQGVGGHAFVIGDAGGFN 426
Db 294 ENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGVGGHAFVIGDAGGFN 353
QY 427 HVNWMGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
Db 354 HVNWMGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 395

RESULT 4
US-10-002-784A-24
; Sequence 24, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:44:58 ; Search time 145.152 Seconds
(without alignments)
1305.574 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDDPPSQLHRSSLVKNLQ.....ALGTGGAGGFGNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/us07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	468	14	US-10-002-784A-27
2	1332	53.3	248	14	US-10-002-784A-25
3	1327.5	53.1	398	16	US-10-428-817A-164
4	1324.5	53.0	398	14	US-10-002-784A-24
5	1323.5	52.9	398	16	US-10-474-792-642
6	1316.5	52.7	371	17	US-10-872-198-25
7	1316.5	52.7	371	17	US-10-872-197A-25
8	1316.5	52.7	371	20	US-11-021-951-25
9	1168	46.7	220	14	US-10-002-784A-26
10	1136	45.4	251	8	US-08-882-431-16
11	1136	45.4	251	14	US-10-002-784A-16

12	1136	45.4	251	17	US-10-767-687-16	Sequence 16, Appl
13	1129	45.2	251	16	US-10-428-817A-163	Sequence 163, Appl
14	1122	44.9	251	8	US-08-973-391A-13	Sequence 13, Appl
15	1122	44.9	251	9	US-09-308-830-13	Sequence 13, Appl
16	938.5	37.5	250	9	US-09-870-759-20	Sequence 20, Appl
17	938.5	37.5	250	10	US-09-751-708A-20	Sequence 20, Appl
18	938.5	37.5	250	16	US-10-428-817A-16	Sequence 16, Appl
19	938.5	37.5	250	17	US-10-937-758A-20	Sequence 20, Appl
20	543	21.7	239	9	US-09-150-947B-12	Sequence 12, Appl
21	543	21.7	239	14	US-10-172-425B-12	Sequence 12, Appl
22	541	21.6	238	16	US-10-428-817A-183	Sequence 183, Appl
23	541	21.6	255	15	US-10-354-948-2	Sequence 2, Appl
24	541	21.6	266	9	US-09-870-759-10	Sequence 10, Appl
25	541	21.6	266	10	US-09-751-708A-10	Sequence 10, Appl
26	541	21.6	266	16	US-10-428-817A-6	Sequence 6, Appl
27	541	21.6	266	17	US-10-937-758A-10	Sequence 10, Appl
28	539	21.6	266	14	US-10-151-336-8	Sequence 8, Appl
29	532	21.3	266	14	US-10-002-784A-6	Sequence 6, Appl
30	532	21.3	266	17	US-10-767-687-6	Sequence 6, Appl
31	530	21.2	239	14	US-10-002-784A-10	Sequence 10, Appl
32	530	21.2	239	17	US-10-767-687-10	Sequence 10, Appl
33	525	21.0	239	8	US-08-882-431-10	Sequence 10, Appl
34	523	20.9	266	14	US-10-002-784A-8	Sequence 8, Appl
35	523	20.9	266	17	US-10-767-687-8	Sequence 8, Appl
36	514	20.6	266	8	US-08-882-431-14	Sequence 14, Appl
37	514	20.6	266	14	US-10-002-784A-14	Sequence 14, Appl
38	514	20.6	266	17	US-10-767-687-14	Sequence 14, Appl
39	513.5	20.5	265	8	US-08-882-431-6	Sequence 6, Appl
40	513	20.5	240	17	US-10-923-324-4	Sequence 4, Appl
41	513	20.5	266	16	US-10-428-817A-186	Sequence 186, Appl
42	510	20.4	239	16	US-10-428-817A-185	Sequence 185, Appl
43	509	20.4	240	17	US-10-923-324-1	Sequence 1, Appl
44	509	20.4	266	9	US-09-870-759-12	Sequence 12, Appl
45	509	20.4	266	10	US-09-751-708A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR FILING DATE: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion
US-10-002-784A-27

Query Match	100.0%;	Score 2500;	DB 14;	Length 468;
Best Local Similarity	100.0%;	Pred. No. 2.8e-178;		
Matches 468;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQRSHDLIYNVSGPNYDKLK	60	
Db	1	MQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQRSHDLIYNVSGPNYDKLK	60	
Qy	61	TELKNQEMATLFDKKNIDYGVYVHLVCLCENASRSACIGGVTVNREGNHLIPKKIVVK	120	
Db	61	TELKNQEMATLFDKKNIDYGVYVHLVCLCENASRSACIGGVTVNREGNHLIPKKIVVK	120	

Patent No. 6692746
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/09/708, 008B
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US/08/896,933
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 08/252,978
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 220
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-09-708-008B-20

Query Match 37.5%; Score 938.5; DB 4; Length 220;
Best Local Similarity 84.9%; Pred. No. 5.5e-75;
Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;
QY 5 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLTELK 64
Db 4 PKPSQLQRNLVKTETKIIYIFFMRVTLVTHENVKSVQDLRSHDLIYNVSGPNYDKLTELK 63
QY 65 NQEMATLFDKNDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPKKIVVKVSI 123
Db 64 NQEMATLFDKNDIYGVYHYHLCYLCEAERSACIYGGVTNREGNHLIPKKIVVKVSI 123
QY 124 DGQISLSDIETNKKMVTAEQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKNKESFW 183
Db 124 DGQISLSDIETNKKMVTAEQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKNKESFW 183
QY 184 FDFPPEFTQSKYLMYKDNETLDSNT-QIEVYLTK 220
Db 183 FDFPPEFTQSKYLMYKDNETLDSNTQIEVYLTK 220

Search completed: September 17, 2005, 00:48:31
Job time : 27.0362 secs

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-2

Query Match 21.6%; Score 541; DB 1; Length 255;
Best Local Similarity 47.7%; Pred. No. 1.1e-39;
Matches 113; Conservative 39; Mismatches 67; Indels 18; Gaps 7;
QY 2 QQDDPPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGP---NYD 57
Db 19 QPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGYD 78
QY 58 KLKTELKNOEMATLFDKNDIYGVYHYHLCYLCEA-----ERSACI-GGVTNRE 107
Db 79 NVRVFKNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCMYGGVTEHN 138
QY 108 GNHLEIPKKIVVKVSIIDGSIQSLSPDIETNKKMVTAEQELDYKVRKYLTNDKQLYTNGPSKY 167
Db 139 GNQLDKYRSITVRVFEDEGKNLLSFDVQTNKKKVTAEQLDYLTRHYLVKRNKLYEFNNSPY 198
QY 168 ETGYIKFIPKNKESFWDFPPEP--EFTQSKYLMYKDNETLDS-NTQIEVYLTKQ 221
Db 199 ETGYIKFI-ENENSPWYDMWPAPGDKFDQSKYLMYNDNKKWYDSKDKVIEVYLTKK 254

Search completed: September 17, 2005, 00:48:31
Job time : 27.0362 secs

RESULT 15
US-08-446-918A-2
Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223

THIS PAGE BLANK (USPTO)


```
Db 181 SFWDFPPEFTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 11
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoeher, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-13

Query Match 44.9%; Score 1122; DB 4; Length 251;
Best Local Similarity 97.3%; Pred. No. 3.9e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QDDPDSQLHRSLLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVSGPNYDKLTK 61
Db 31 QDDPDSQLHRSLLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVSGPNYDKLTK 90
QY 62 ELKNQMATLFDKNDIYGYEYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIYVVK 120
Db 91 ELKNQMATLFDKNDIYGYEYHLCYLCEAERSACIYGGVTHNEGNHLIPIPKIYVVK 150
QY 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKE 180
Db 151 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKE 210
QY 181 SFWDFPPEFTQSKYLMYKDNETLDSNT-QIEVYLTK 220
Db 211 SFWDFPPEFTQSKYLMYKDNETLDSNTSQIEVYLTK 251

RESULT 12
US-08-896-933-20
; Sequence 20, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20

Query Match 37.5%; Score 938.5; DB 3; Length 220;
Best Local Similarity 84.9%; Pred. No. 5.5e-75;
Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;

QY 5 PDPSSLHRSLLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVSGPNYDKLTK 64
Db 4 PKPSQLQRSNLVKTFKIYIFMRVTLVTHENVKSDQLRSHDLIYVSGPNYDKLTK 63
QY 65 NOEMATLFDKNDIYGYEYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIYVVKSI 123
Db 64 NOEMATLFDKNDIYGYEYHLCYLCEAERSACLYGGVTHNEGNHLIPIPKIYVVKSI 123
QY 124 DGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKESFW 183
Db 124 DGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKESFW 182
QY 184 FDFPPEFTQSKYLMYKDNETLDSNT-QIEVYLTK 220
Db 183 FDFPPEFTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 14
US-09-708-008B-20
; Sequence 20, Application US/09708008B
```

Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220
Db 181 SFWDFLPEPEFTQSKYLMYKONETLDSNTSQIEVYLTK 221

RESULT 8

US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 44.9%; Score 1123; DB 3; Length 221;
Best Local Similarity 97.3%; Pred. No. 2.6e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
QY 62 ELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI-GGVTNREGNHLEIPKKIVVK 120
Db 61 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220
Db 181 SFWDFLPEPEFTQSKYLMYKONETLDSNTSQIEVYLTK 221

RESULT 9

US-09-708-008B-29
; Sequence 29, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; EARLIER APPLICATION NUMBER: 08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978

; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-29

Query Match 44.9%; Score 1123; DB 4; Length 221;
Best Local Similarity 97.3%; Pred. No. 2.6e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
QY 62 ELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI-GGVTNREGNHLEIPKKIVVK 120
Db 61 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220
Db 181 SFWDFLPEPEFTQSKYLMYKONETLDSNTSQIEVYLTK 221

RESULT 10

US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 44.9%; Score 1122; DB 4; Length 221;
Best Local Similarity 97.3%; Pred. No. 3.2e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
QY 62 ELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI-GGVTNREGNHLEIPKKIVVK 120
Db 61 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220

```
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16

Query Match 45.4%; Score 1136; DB 3; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.2e-92;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
Db 31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCENASACI-GGVTNREGNHLIPIPKIVVK 120
Db 91 ELKQEMATLFDKKNVDIYGVVEYHLCYLCENASACIYGGVTNHEGHNHLIPIPKIVVK 150
QY 121 VSDIGIQSLSFDIETNKKMVTAAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 151 VSDIGIQSLSFDIETNKKMVTAAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSIEVYLTTK 251

RESULT 6
US-08-882-431B-16
; Sequence 16, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
```

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-16

Query Match 45.4%; Score 1136; DB 4; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.2e-92;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
Db 31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCENASACI-GGVTNREGNHLIPIPKIVVK 120
Db 91 ELKQEMATLFDKKNVDIYGVVEYHLCYLCENASACIYGGVTNHEGHNHLIPIPKIVVK 150
QY 121 VSDIGIQSLSFDIETNKKMVTAAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 151 VSDIGIQSLSFDIETNKKMVTAAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSIEVYLTTK 251

RESULT 7
US-08-896-933-29
; Sequence 29, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
; US-08-896-933-29

Query Match 44.9%; Score 1123; DB 3; Length 221;
Best Local Similarity 97.3%; Pred. No. 2.6e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
Db 1 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 60
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCENASACI-GGVTNREGNHLIPIPKIVVK 120
Db 61 ELKQEMATLFDKKNVDIYGVVEYHLCYLCENASACIYGGVTNHEGHNHLIPIPKIVVK 120
QY 121 VSDIGIQSLSFDIETNKKMVTAAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
```

```
;
;
; AUTHORS: Hamrick, M. R.
; AUTHORS: Hamill, R. J.
; AUTHORS: Patti, J. M.
; AUTHORS: Musser, J. M.
; TITLE: A conserved Streptococcus pyogenes
; TITLE: extracellular cysteine protease cleaves human
; TITLE: fibronectin and degrades vitronectin
; JOURNAL: Microb. Pathog.
; VOLUME: 15
; PAGES: 327-346
; DATE: 1993
;
PCT-US95-11723-5

Query Match          53.1%; Score 1327.5; DB 5; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

Qy 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNLLTPVI 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 FMES-YVEQIKENKKLDT-----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPNLLTPVI 173

Qy 249 EKVKPGESQFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 174 EKVKPGESQFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 233

Qy 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRSRVORALK 368
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRSRVORALK 293

Qy 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQG-GKVGGHAFVIDGADGRNFY 426
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 294 ENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGVGVGVGGHAFVIDGADGRNFY 353

Qy 427 HVNWGCVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 354 HVNWGCVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395

RESULT 4
PCT-US96-05997-1
; Sequence 1, Application PC/TUS9605997
; GENERAL INFORMATION:
; APPLICANT: Musser M.D., James M.
; APPLICANT: Kapur M.D., Vivek
; APPLICANT: Ananthaswamy, H. N.
; APPLICANT: Fernandez, A.
; TITLE OF INVENTION: Use of extracellular cysteine protease
; TITLE OF INVENTION: to inhibit cell proliferation
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEIL, GOTSHAL & MANGES
; STREET: 2882 Sand Hill Road, Suite 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025-7022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,542
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,965
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter Ph.D., Barbara

;
;
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: BAYL-004/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pyogenes
; STRAIN: MGAS 1719
; IMMEDIATE SOURCE:
; CLONE: speB7
;
PCT-US96-05997-1

Query Match          53.1%; Score 1327.5; DB 5; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

Qy 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNLLTPVI 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 FMES-YVEQIKENKKLDT-----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPNLLTPVI 173

Qy 249 EKVKPGESQFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 174 EKVKPGESQFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 233

Qy 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRSRVORALK 368
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRSRVORALK 293

Qy 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQG-GKVGGHAFVIDGADGRNFY 426
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 294 ENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGVGVGVGGHAFVIDGADGRNFY 353

Qy 427 HVNWGCVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 354 HVNWGCVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395

RESULT 5
US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
```

```

; STRAIN: MGAS 1719
; IMMEDIATE SOURCE:
; CLONE: SPEB7 (cysteine protease)
; PUBLICATION INFORMATION:
; AUTHORS: Kapur, V.
; AUTHORS: Topouzis, S.
; AUTHORS: Majesky, M. W.
; AUTHORS: Li, L.-L.
; AUTHORS: Hamrick, M. R.
; AUTHORS: Hamill, R. J.
; AUTHORS: Patti, J. M.
; AUTHORS: Musser, J. M.
; TITLE: A conserved Streptococcus pyogenes
; TITLE: extracellular cysteine protease cleaves human
; TITLE: fibronectin and degrades vitronectin
; JOURNAL: Microb. Pathog.
; VOLUME: 15
; PAGES: 327-346
; DATE: 1993
; US-08-931-220-5

Query Match      53.1%; Score 1327.5; DB 3; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDT-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173

QY 249 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLPA 308
DB 174 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLPA 233

QY 309 AISTROYNNNLPITYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRVQRAALK 368
DB 234 AISTROYNNNLPITYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRVQRAALK 293

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYVYOG-GKVGGHAFVIDGADGRNPFY 426
DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYVYQGVGVKGKGFHAFVIDGADGRNPFY 353

QY 427 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 468
DB 354 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 395

RESULT 3
PCT-US95-11723-5
; Sequence 5, Application PC/TUS9511723
; GENERAL INFORMATION:
; APPLICANT: Musser M.D., James M.
; APPLICANT: Kapur M.D., Vivek
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Identifying Streptococcus
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAW OFFICES OF BARBARA RAE-VENTER
; STREET: P.O. Box 60039
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-SEP-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,542
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter Ph.D., Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: BAYL-004/03US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6205
; TELEFAX: (415) 424-8760
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pyogenes
; STRAIN: MGAS 1719
; IMMEDIATE SOURCE:
; CLONE: SPEB7 (cysteine protease)
; PUBLICATION INFORMATION:
; AUTHORS: Kapur, V.
; AUTHORS: Topouzis, S.
; AUTHORS: Majesky, M. W.
; AUTHORS: Li, L.-L.

; STRAIN: MGAS 1719
; IMMEDIATE SOURCE:
; CLONE: SPEB7 (cysteine protease)
; PUBLICATION INFORMATION:
; AUTHORS: Kapur, V.
; AUTHORS: Topouzis, S.
; AUTHORS: Majesky, M. W.
; AUTHORS: Li, L.-L.
; AUTHORS: Hamrick, M. R.
; AUTHORS: Hamill, R. J.
; AUTHORS: Patti, J. M.
; AUTHORS: Musser, J. M.
; TITLE: A conserved Streptococcus pyogenes
; TITLE: extracellular cysteine protease cleaves human
; TITLE: fibronectin and degrades vitronectin
; JOURNAL: Microb. Pathog.
; VOLUME: 15
; PAGES: 327-346
; DATE: 1993
; US-10-030-330-6

Query Match      53.1%; Score 1327.5; DB 4; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDT-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173

QY 249 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLPA 308
DB 174 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLPA 233

QY 309 AISTROYNNNLPITYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRVQRAALK 368
DB 234 AISTROYNNNLPITYSGRESNVQKMAISELMADVIGISVDMYDGPSSGSGSSRVQRAALK 293

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYVYOG-GKVGGHAFVIDGADGRNPFY 426
DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYVYQGVGVKGKGFHAFVIDGADGRNPFY 353

QY 427 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 468
DB 354 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 395

RESULT 2
US-10-030-330-6
; Sequence 6, Application US/10030330
; Patent No. 6833262
; GENERAL INFORMATION:
; APPLICANT: The University of Georgia Research Foundation, Inc
; TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN
; FILE REFERENCE: 235.00210201
; CURRENT APPLICATION NUMBER: US/10/030,330
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/130,436
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
; US-10-030-330-6

Query Match      53.1%; Score 1327.5; DB 4; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDT-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:42:17 ; Search time 26.0362 Seconds
(without alignments)
1341.817 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDPDPSSLHRSLLVKNLQ.....ALCTGGGAGFNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6C COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1327.5	53.1	398	3	US-08-931-220-5
2	1327.5	53.1	398	4	US-10-030-330-6
3	1327.5	53.1	398	5	PCT-US95-11723-5
4	1327.5	53.1	398	5	PCT-US96-05997-1
5	1136	45.4	251	3	US-09-144-776B-16
6	1136	45.4	251	4	US-08-882-431B-16
7	1123	44.9	221	3	US-08-896-933-29
8	1123	44.9	221	3	US-09-314-235-29
9	1123	44.9	221	4	US-09-708-008B-29
10	1122	44.9	221	4	US-08-973-391C-14
11	1122	44.9	221	4	US-08-973-391C-13
12	938.5	37.5	220	3	US-08-896-933-20
13	938.5	37.5	220	3	US-09-314-235-20
14	938.5	37.5	220	4	US-09-708-008B-20
15	541	21.6	255	1	US-08-446-918A-2
16	541	21.6	255	2	US-08-580-806-2
17	539	21.6	266	3	US-09-414-276-8
18	532	21.3	266	3	US-09-144-776B-6
19	532	21.3	266	4	US-08-882-431B-6
20	530	21.2	239	3	US-09-144-776B-10
21	530	21.2	239	4	US-08-882-431B-10
22	528	21.1	239	3	US-08-896-933-26
23	528	21.1	239	3	US-09-314-235-26
24	528	21.1	239	4	US-09-708-008B-26
25	523	20.9	266	3	US-09-144-776B-8
26	523	20.9	266	4	US-08-882-431B-8
27	514	20.6	266	3	US-09-144-776B-14

28	514	20.6	266	4	US-08-882-431B-14
29	510	20.4	238	3	US-08-896-933-28
30	510	20.4	238	3	US-09-314-235-28
31	510	20.4	238	4	US-09-708-008B-28
32	509	20.4	239	3	US-08-896-933-27
33	509	20.4	239	3	US-09-314-235-27
34	509	20.4	239	4	US-09-708-008B-27
35	489	19.6	239	3	US-08-896-933-21
36	489	19.6	239	3	US-09-314-235-21
37	489	19.6	239	4	US-09-708-008B-21
38	414	16.6	840	4	US-10-030-330-5
39	397.5	15.9	79	3	US-09-144-776B-24
40	397.5	15.9	79	4	US-08-882-431B-24
41	393	15.7	843	4	US-10-030-330-1
42	295.5	11.8	228	3	US-08-896-933-25
43	295.5	11.8	228	3	US-09-314-235-25
44	295.5	11.8	228	4	US-09-708-008B-25
45	257.5	10.3	233	1	US-08-446-918A-4

ALIGNMENTS

RESULT 1
US-08-931-220-5
; Sequence 5, Application US/08931220
; Patent No. 6030835
; GENERAL INFORMATION:
; APPLICANT: Musser M.D., James M.
; APPLICANT: Kapur M.D., Vivek
; TITLE OF INVENTION: Methods and Compositions for Identifying
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSES: WEIL, GOTSHAL & MANGES
; STREET: 2882 Sand Hill Road, Suite 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025-7022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,220
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,542
; FILING DATE: 14-SEP-1994
; APPLICATION NUMBER: US 08/160,965
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter Ph.D., Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: BAYL-004/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pyogenes

PF 20-APR-2000; 2000WO-US010574.
XX
XX 21-APR-1999; 99US-0130436P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (TRAV/) TRAVIS J.
PA (POTE/) POTEMPA J.
PA (NELS/) NELSON D.
XX
XX
PI Travis J, Potempa J, Nelson D;
XX
XX WPI; 2000-679600/66.
XX
XX Novel oral bacterial periodontain polypeptide for treating periodontal
PT diseases, has amidolytic activity for cleavage of non-denatured human
PT alphas-proteinase inhibitor at reactive site loop region of inhibitor.
XX
XX Example 1; Fig 1; 55pp; English.
XX
XX The present sequence is given in a specification relating to novel oral
CC bacterial polypeptide referred to as periodontain. The polypeptide has
CC amidolytic activity for cleavage of denatured polypeptides and non-
CC denatured serpin polypeptides. It has amidolytic activity for cleavage of
CC a non-denatured human alpha 1-proteinase inhibitor at a reactive site
CC loop region of the inhibitor. Periodontain is useful for inhibiting the
CC peptidase activity and reducing periodontitis, loss of tooth attachment
CC and periodontal pocket formation, and for reducing growth of bacteria,
CC preferably P. gingivalis in vitro or in vivo. It is useful for protecting
CC an animal from a disease caused by P. gingivalis and for treating
CC periodontal diseases, including gingivitis and periodontitis
XX
XX Sequence 398 AA;
Query Match 47.8%; Score 1195.5; DB 3; Length 398;
Best Local Similarity 84.0%; Pred. No. 1.3e-88;
Matches 237; Conservative 5; Mismatches 29; Indels 11; Gaps 5;
QY 192 FTQSKYLMYIKDNETLDSNTQIEVLT---KQPVVKSLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDI-----TYAGTAIEIKQPVKSLDSKGIHYNQGNPNYLLTPXX 173
QY 249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNKGLXDYTYTLSSNNPYNFHPKNLFA 308
DB 174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNKGLXKYTYTLSSNNPYNFHPKNLXX 233
QY 309 AISTROYNNILPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGAGSSRVQALX 368
DB 234 XISTROYNNILPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGAGSSRVQALX 293
QY 369 ENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFX 426
DB 294 ENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFX 353
QY 427 HYNMGWGGYSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 468
DB 354 HYNMGWGGYSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 395

Search completed: September 17, 2005, 01:09:43
Job time : 154.962 secs

CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins
 XX Sequence 398 AA;

Query Match 52.9%; Score 1323.5; DB 5; Length 398;
 Best Local Similarity 91.1%; Pred. No. 4.6e-99;
 Matches 257; Conservative 5; Mismatches 9; Indels 11; Gaps 5;
 QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGHYNQGNPNYLLTPVI 248
 Db 120 FMES-YVEQIKENKKLDT-----TYAGTAETKQPVVKSLLDSKGHYNQGNPNYLLTPVI 173
 QY 249 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPNYFNHPKNLFA 308
 Db 174 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPNYFNHPKNLFA 233
 QY 309 AISTROYNNNLTPTSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 368
 Db 234 AISTROYNNNLTPTSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 293
 QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFI 426
 Db 294 ENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGGKVGGHAFVIDGADGRNFI 353
 QY 427 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
 Db 354 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 395

RESULT 12
 AAE37685
 ID AAE37685 standard; protein; 398 AA.
 AC AAE37685;
 XX
 XX 06-OCT-2003 (first entry)
 XX
 XX Streptococcus pyogenes pyrogenic exotoxin B (SpeB) protein.
 DE
 XX Superantigen toxin; vaccine; infection; pyrogenic exotoxin B; SpeB;
 KW gene therapy.
 XX
 XX Streptococcus pyogenes.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..145
 FT /label= Signal_peptide
 FT Protein 146..398
 FT /note= "S. pyogenes mature SpeB protein"
 XX
 XX WO2003056015-A1.
 XX
 XX 10-JUL-2003.
 XX
 XX 26-NOV-2001; 2001WO-US046540.
 PF
 XX 26-NOV-2001; 2001US-00002784.
 PR
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 PA
 XX

PI Ulrich RG;
 XX WPI; 2003-492125/46.
 DR
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 XX Example 14; Page 133; 141pp; English.

XX The invention provides a superantigen toxin DNA fragment which has been
 CC genetically altered such that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is disrupted or
 CC altered. DNA fragments of the invention are useful in the production of
 CC vaccines against bacterial superantigen toxin infections. They are also
 CC useful in gene therapy. The present sequence is Streptococcus pyogenes
 CC pyrogenic exotoxin B (SpeB) protein. This sequence is used in the
 CC invention

XX Sequence 398 AA;

Query Match 52.9%; Score 1323.5; DB 7; Length 398;
 Best Local Similarity 91.1%; Pred. No. 4.6e-99;
 Matches 257; Conservative 5; Mismatches 9; Indels 11; Gaps 5;
 QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGHYNQGNPNYLLTPVI 248
 Db 120 FMES-YVEQIKENKKLDT-----TYAGTAETKQPVVKSLLDSKGHYNQGNPNYLLTPVI 173
 QY 249 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPNYFNHPKNLFA 308
 Db 174 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPNYFNHPKNLFA 233
 QY 309 AISTROYNNNLTPTSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 368
 Db 234 AISTROYNNNLTPTSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 293
 QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFI 426
 Db 294 ENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGGKVGGHAFVIDGADGRNFI 353
 QY 427 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
 Db 354 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 395

RESULT 13
 ADR83971
 ID ADR83971 standard; protein; 398 AA.
 XX
 XX ADR83971;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX S. pyogenes hyperimmune system reactive antigen Spy2039.
 DE
 XX hyperimmune serum reactive antigen; vaccine; anticaline.
 KW
 XX Streptococcus pyogenes.
 OS
 XX WO2004078907-A2.
 PN
 XX 16-SEP-2004.
 PD
 XX 02-MAR-2004; 2004WO-EP002087.
 PF
 XX 04-MAR-2003; 2003EP-00450061.
 PR
 XX (INTE-) INTERCELL AG.
 PA
 XX Meinke A, Nagy E, Winkler B, Gelbmann D;
 PI WPI; 2004-653698/63.
 XX N-PSDB; ADR83821.
 DR


```

XX OS Streptococcus pyogenes.
XX PN US6030835-A.
XX PD 29-FEB-2000.
XX PF 16-SEP-1997; 97US-00931220.
XX PR 02-DEC-1993; 93US-00160965.
XX PR 14-SEP-1994; 94US-00306542.
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX PI Kapur V, Musser JM;
XX DR N-PSDB; AAA07111.
XX PT Determining the presence of a Group A Streptococcus expressing a protease
XX PT capable of degrading proteins of the extracellular matrix, using a
XX PT specific antibody.
XX PS Disclosure; Col 7-8; 56pp; English.
XX CC This sequence represents the S. pyogenes cysteine protease speB7. The
XX CC invention relates to a method for determining the presence of a Group A
XX CC Streptococcus which expresses an extracellular protease (preferably speB)
XX CC capable of degrading proteins of the extracellular matrix, comprising:
XX CC (1) combining a sample with an assay medium comprising a first member of
XX CC a specific binding pair which binds to a second member of the binding
XX CC pair to form a complex, where the first member has at least 1 epitopic
XX CC site competitive with at least 1 conserved epitopic site on the protease;
XX CC and (2) detecting complex formation as indicative of the presence of the
XX CC pathogenic organism. The method is useful for screening host samples for
XX CC evidence of infection with Streptococcus pyogenes and for monitoring the
XX CC disease status of the host. The speB gene products are used as a vaccine
XX CC for protecting against Streptococcus mediated diseases such as
XX CC pharyngitis, tonsillitis, skin infections, scarlet fever, sepsis,
XX CC erysipelas, fasciitis, pneumonia, acute rheumatic fever,
XX CC poststreptococcal glomerulonephritis, cellulitis, bacteraemia, and
XX CC meningitis
XX SQ Sequence 398 AA;

Query Match 53.1%; Score 1327.5; DB 3; Length 398;
Best Local Similarity 91.5%; Pred. No. 2.2e-99;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIIHYNGNPYNLLTPVI 248
DB 120 FMES-YVEQIKENKKLDT-----TYAGTAIEIKQPVVKSLLDSKGIIHYNGNPYNLLTPVI 173

QY 249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 308
DB 174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 233

QY 309 AISTROYNNNIIPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRRVQALX 368
DB 234 AISTROYNNNIIPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRRVQALX 293

QY 369 ENFGYNQSVHQINRSDFS--QDWEAQIDKELSONQPVYQOG--GKVGGHAFVIGADGRNRY 426
DB 294 ENFGYNQSVHQINRSDFS--QDWEAQIDKELSONQPVYQOG--GKVGGHAFVIGADGRNRY 353

QY 427 HVNMGVGGVSDGFFRLDALNPSALGTGGAGGFGNGQSAVVG 468
DB 354 HVNMGVGGVSDGFFRLDALNPSALGTGGAGGFGNGQSAVVG 395

RESULT 9
ADF89840
ID ADF89840 standard; protein; 398 AA.

```

```

XX ADF89840;
XX AC 26-FEB-2004 (first entry)
XX DT Streptococcal pyrogenic exotoxin B (SpEB) sequence.
XX DE Superantigen; SAG; enterotoxin; cytostatic; gene therapy; cancer;
XX KW pyrogenic exotoxin; SpE; SpEB.
XX OS Streptococcus sp.
XX PN WO2003094846-A2.
XX PD 20-NOV-2003.
XX PF 08-MAY-2003; 2003WO-US014381.
XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0406750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX (TERM/) Terman D S.
XX PA Terman DS;
XX PI WPI; 2004-011997/01.
XX DR Treating a subject with cancer or malignant diseases comprises
XX DR intratumoral, intrathecal or intracavitary administration of an amount of
XX DR a superantigen composition to the subject.
XX PS Disclosure; SEQ ID NO 17; 91pp; English.
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Streptococcal pyrogenic exotoxin B (SpEB).
XX SQ Sequence 398 AA;

Query Match 53.1%; Score 1327.5; DB 8; Length 398;
Best Local Similarity 91.5%; Pred. No. 2.2e-99;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIIHYNGNPYNLLTPVI 248
DB 120 FMES-YVEQIKENKKLDT-----TYAGTAIEIKQPVVKSLLDSKGIIHYNGNPYNLLTPVI 173

QY 249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 308
DB 174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 233

QY 309 AISTROYNNNIIPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRRVQALX 368
DB 234 AISTROYNNNIIPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRRVQALX 293

QY 369 ENFGYNQSVHQINRSDFS--QDWEAQIDKELSONQPVYQOG--GKVGGHAFVIGADGRNRY 426
DB 294 ENFGYNQSVHQINRSDFS--QDWEAQIDKELSONQPVYQOG--GKVGGHAFVIGADGRNRY 353

```

XX The present sequence is the *Streptococcus pyogenes* clone speB7 pre-pro
 CC cysteine protease (CP), which can be used to inhibit neoplastic cell
 CC proliferation, especially in a human, useful in the treatment of
 CC neoplastic conditions, e.g. carcinomas, sarcomas, melanomas, lymphomas
 CC and leukemias originating from blood, lung, mammary gland, prostate,
 CC intestine, stomach, liver, heart, skin, pancreas or brain tissue. The CP
 CC is especially associated with a wound covering, and can also be used to
 CC prevent metastasis or identify susceptible neoplastic cells. K1735 and
 CC CM519 melanoma cells were injected s.c. into nu/nu mice, optionally
 CC followed by i.p. injection of CP (100 microg, 24 hours later). The mice
 CC were checked twice weekly for tumour growth for 12 weeks, to give results
 CC that showed that treatment with CP completely protected athymic mice
 CC against transplanted K1735 melanoma growth, and protected 60% of the mice
 CC from developing CM519 melanomas

XX SQ Sequence 398 AA;

Query Match 53.1%; Score 1327.5; DB 2; Length 398;
 Best Local Similarity 91.5%; Pred. No. 2.2e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIHYNQGNPNLLTPVI 248
 DB 120 FMES-YVEQIKENKKLDT-----TYAGTAIEIKQPVVKSLLDSKGIHYNQGNPNLLTPVI 173
 QY 249 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNHPKNLFA 308
 DB 174 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNHPKNLFA 233
 QY 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRVQALK 368
 DB 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRVQALK 293
 QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQOG-GKVGGHAFVIDGADGRNFI 426
 DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVKGVGGHAFVIDGADGRNFI 353
 QY 427 HVNWGCGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
 DB 354 HVNWGCGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 395

RESULT 7

AAR95856
 ID AAR95856 standard; protein; 398 AA.

XX AAR95856;

XX 30-OCT-1996 (first entry)

XX S. *pyogenes* speB gene encoded extracellular protease.

XX Immunogenic peptide; speB gene; extracellular protease; production;
 KW antibody; vaccine; diagnosis; detection; *Streptococcus* infection;
 KW group A; prevention; treatment; pharyngitis; tonsillitis; skin infection;
 KW acute rheumatic fever; scarlet fever; probe;
 KW post-streptococcal glomerulonephritis; sepsis; meningitis; erysipellis;
 KW cellulitis; fasciitis; toxic shock like syndrome.

XX *Streptococcus pyogenes*.

XX Key Location/Qualifiers
 FH Misc-difference 216
 FT /note= "corresponding codon TAG"

FT Domain 333..338
 FT /label= putative nucleotide binding domain

FT Region 382..398
 FT /label= potential collagen docking region

XX WO9608569-A2.

XX 21-MAR-1996.

XX 13-SEP-1995; 95WO-US011723.
 PF 14-SEP-1994; 94US-00306542.
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Musser JA, Kapur V;
 PI WPI; 1996-179944/18.
 XX N-PSDB; AAT15294.
 DR Use of extracellular protease(s), partic. cysteine protease - for
 PT detection, diagnosis prevention and treatment of infection by pathogenic
 PT organisms, partic. gp. A *streptococcus* strains.
 XX Disclosure; Page 12; 97pp; English.

XX The present sequence is the *S. pyogenes* speB gene encoded extracellular
 CC protease. An immunogenic peptide derived from the protease can be used in
 CC the prodn. of antibody (Ab) and vaccine. Ab is prepd. by introducing the
 CC peptide into a mammal, pref. a mouse, followed by Ab isolation. The Ab or
 CC a probe derived from the gene can be used for the diagnosis and detection
 CC of gp. A *Streptococcus* infections, while vaccine, which inhibits
 CC streptococcal replication, can be used to prevent and treat gp. A
 CC *Streptococcus* infections, and partic. to ameliorate pharyngitis,
 CC tonsillitis, skin infections, acute rheumatic fever, scarlet fever, post-
 CC streptococcal glomerulonephritis, sepsis, meningitis, erysipellis,
 CC cellulitis, fasciitis and toxic shock like syndrome

XX SQ Sequence 398 AA;

Query Match 53.1%; Score 1327.5; DB 2; Length 398;
 Best Local Similarity 91.5%; Pred. No. 2.2e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIHYNQGNPNLLTPVI 248
 DB 120 FMES-YVEQIKENKKLDT-----TYAGTAIEIKQPVVKSLLDSKGIHYNQGNPNLLTPVI 173
 QY 249 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNHPKNLFA 308
 DB 174 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYNHPKNLFA 233
 QY 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRVQALK 368
 DB 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRVQALK 293
 QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQOG-GKVGGHAFVIDGADGRNFI 426
 DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVKGVGGHAFVIDGADGRNFI 353
 QY 427 HVNWGCGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
 DB 354 HVNWGCGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 395

RESULT 8

AAY81812
 ID AAY81812 standard; protein; 398 AA.

XX AAY81812;

XX 09-JUN-2000 (first entry)

XX S. *pyogenes* cysteine protease speB7 protein sequence.

XX Cysteine protease; speB; Group A *Streptococcus*; extracellular protease;
 KW detection; diagnosis; extracellular matrix; infection; skin infection;
 KW disease status monitoring; vaccine; *Streptococcus* mediated disease;
 KW pharyngitis; tonsillitis; scarlet fever; sepsis; erysipellis; fasciitis;
 KW pneumonia; acute rheumatic fever; poststreptococcal glomerulonephritis;
 KW cellulitis; bacteraemia; meningitis.

CC (SpeB). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the wild-type SpeB mature protein

XX SQ Sequence 248 AA;
Query Match 53.3%; Score 1332; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 4.7e-100;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 221 QPVKSLDLSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 280
Db 1 QPVKSLDLSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 60
QY 281 YPNKGLKDYTYTLSSNNPFNFHKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 340
Db 61 YPNKGLKDYTYTLSSNNPFNFHKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 120
QY 341 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSON 400
Db 121 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSON 180
QY 401 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 460
Db 181 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 240
QY 461 GYQSAVVG 468
Db 241 GYQSAVVG 248

RESULT 5
AAE37686
ID AAE37686 standard; protein; 248 AA.
XX AC AAE37686;
XX DT 06-OCT-2003 (first entry)
XX DE Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) protein.
XX KW Superantigen toxin; vaccine; infection; pyrogenic exotoxin B; SpeB;
XX KM Gene therapy.
XX OS Streptococcus pyogenes.
XX PN WO2003056015-A1.
XX PD 10-JUL-2003.
XX PF 26-NOV-2001; 2001WO-US046540.
XX PR 26-NOV-2001; 2001US-00002784.
XX (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX PA Ulrich RG;
XX PI WPI; 2003-492125/46.
XX DR New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX PS Example 14; Page 134; 141pp; English.
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is Streptococcus pyogenes
XX mature pyrogenic exotoxin B (SpeB) protein. This sequence is used in the
XX invention

XX SQ Sequence 248 AA;
Query Match 53.3%; Score 1332; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 4.7e-100;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 221 QPVKSLDLSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 280
Db 1 QPVKSLDLSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 60
QY 281 YPNKGLKDYTYTLSSNNPFNFHKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 340
Db 61 YPNKGLKDYTYTLSSNNPFNFHKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 120
QY 341 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSON 400
Db 121 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSDQWEAQIDKELSON 180
QY 401 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 460
Db 181 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 240
QY 461 GYQSAVVG 468
Db 241 GYQSAVVG 248

RESULT 6
AAW07898
ID AAW07898 standard; protein; 398 AA.
XX AC AAW07898;
XX DT 22-JUL-1997 (first entry)
XX DE Streptococcus pyogenes clone speB7 pre-pro cysteine protease.
XX KW Pre-pro; cysteine; protease; inhibition; neoplastic; proliferation; cell;
XX human; treatment; carcinoma; sarcoma; melanoma; lymphoma; leukaemia;
XX leukemia; blood; lung; mammary gland; prostate; intestine; stomach;
XX liver; heart; skin; pancreas; brain tissue; wound covering; prevention;
XX metastasis; identification; speB7.
XX OS Streptococcus pyogenes.
XX PH Key Location/Qualifiers
XX FT Misc-difference 216 /note= "corresponding codon TAG"
XX FT 333..338
XX FT Domain /label= nucleotide_binding_domain
XX PN WO9634941-A1.
XX PD 07-NOV-1996.
XX PF 30-APR-1996; 96WO-US005997.
XX PR 01-MAY-1995; 95US-00432692.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Musser JM, Kapur V, Ananthaswamy H, Fernandez A;
XX WPI; 1996-506148/50.
XX DR N-PSDB; AAT45219.
XX PT Use of extracellular Streptococcal cysteine protease enzyme - for
XX inhibiting the proliferation of neoplastic cells, e.g. for treating
XX carcinoma, lymphoma or leukaemia.
XX PS Disclosure; Page 59-61; 99pp; English.

RESULT 3
AAE37691
ID AAE37691 standard; protein; 468 AA.
AC AAE37691;
XX
DT 06-OCT-2003 (first entry)
XX
DE S. pyogenes mature mutant SpeA-mature mutant SpeB fusion protein.
XX
KW Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
KW gene therapy; fusion protein; SpeB; mutant; muten.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by GCT"
FT Misc-difference 42 /note= "Wild type Leu substituted with Arg"
FT Misc-difference 267 /note= "Wild type Cys substituted with Ser"
FT
XX WQ2003056015-A1.
XX
PD 10-JUL-2003.
XX
XX 26-NOV-2001; 2001WO-US046540.
XX
PR 26-NOV-2001; 2001US-00002784.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Ulrich RG;
XX
XX WPI; 2003-492125/46.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX
XX Example 14; Page; 141pp; English.
XX
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is Streptococcus pyogenes
XX mature mutant pyrogenic exotoxin A (SpeA)-mature mutant SpeB fusion
XX protein. This sequence is used in the invention. Note: This sequence is
XX not shown in the specification, but is derived from S. pyogenes mature
XX wild-type SpeA-SpeB protein (AAE37684)
XX
SQ Sequence 468 AA;

Query Match 99.4%; Score 2484; DB 7; Length 468;
Best Local Similarity 99.6%; Pred. No. 1.4e-193;
Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQDDPPSQLHRSLLVKNLQNIYFLYEGDPVTHENVKSVQDRSHDLIYNVSGPNYDKLK 60
DB 1 MQDDPPSQLHRSLLVKNLQNIYFLYEGDPVTHENVKSVQDRSHDLIYNVSGPNYDKLK 60

QY 61 TELKNEMATLFDKNDIDYGVYHLCVLCENASRACIGGVNREGNHLEIPKKIVVK 120
DB 61 TELKNEMATLFDKNDIDYGVYHLCVLCENASRACIGGVNREGNHLEIPKKIVVK 120

QY 121 VSDIGIQSLSFDIETNKKMWTAGELDYKVRKYLTDNKLQYTNGPSKYETGYIKFIPKNKE 180
DB 121 VSDIGIQSLSFDIETNKKMWTAGELDYKVRKYLTDNKLQYTNGPSKYETGYIKFIPKNKE 180

QY 181 SFWEDFFPEPFTQSKYLMYYKDNETLDSNTQIEVYLTQKPVVKSLLDSKGHYNOGNP 240
DB 181 SFWEDFFPEPFTQSKYLMYYKDNETLDSNTQIEVYLTQKPVVKSLLDSKGHYNOGNP 240

QY 241 YNLLTPVIEKVPGEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYF 300
DB 241 YNLLTPVIEKVPGEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYF 300

QY 301 NHPKNLFAAISTROYNWNNILPTYSGRESNVOKMAISELMADVIGISVMDYGPSSGSAGS 360
DB 301 NHPKNLFAAISTROYNWNNILPTYSGRESNVOKMAISELMADVIGISVMDYGPSSGSAGS 360

QY 361 SRVQALKENFCVNSVHOINESDFSQDWEAQIDKELSONQPVYQGGKVGGHAFVIDGA 420
DB 361 SRVQALKENFCVNSVHOINESDFSQDWEAQIDKELSONQPVYQGGKVGGHAFVIDGA 420

QY 421 DGRNPFYHNVNMGVSDGPFRLDALNPSALGTGGGAGGFGYQSAVVG 468
DB 421 DGRNPFYHNVNMGVSDGPFRLDALNPSALGTGGGAGGFGYQSAVVG 468

RESULT 4
ABU62333
ID ABU62333 standard; protein; 248 AA.
XX
AC ABU62333;
XX
DT 27-AUG-2003 (first entry)
XX
DE Streptococcus pyrogenic toxin b, wild-type mature sequence.
XX
KW Streptococcus pyrogenic enterotoxin a; vaccine; superantigen toxin; MHC;
KW superantigen-associated bacterial infection; bacterial infection;
KW antibacterial.
XX
OS Streptococcus sp.
XX
PN US2003036644-A1.
XX
PD 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-00002784.
XX
PR 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-00144776.
PA (ULRI/) ULRICH R G.
XX
PI Ulrich RG;
XX
XX WPI; 2003-492125/46.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX
XX Example 14; Page 42-43; 68pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified altered superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection,
XX antisera isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX SEB, SECl) and streptococcal pyrogenic enterotoxin a and b (SPEa and

```

PS Claim 10; Page 44-46; 68pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SpEA and
CC SpEB). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the SpEA L42R/SpEB C47S mutant fusion protein. Note:
CC The present sequence is described as having the Cys to Ser mutation in
CC the SpEB portion at residue 267 (corresponding to amino acid 47 of mature
CC SpEB), but the residue is still Cys
XX
SQ Sequence 468 AA;
Query Match 100.0%; Score 2500; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 6.9e-195;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
Db 1 MQQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
QY 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLPIPKIVVK 120
Db 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLPIPKIVVK 120
QY 121 VSIDGQISLSPDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQISLSPDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDLSKGIHYNQGNP 240
Db 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDLSKGIHYNQGNP 240
QY 241 YNLLTPVIEKVPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
Db 241 YNLLTPVIEKVPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
QY 301 NHPKNLFAAISTROYNNNLPITYSGRESNVQKMAISELMADVGISVDMDYGPSGSGS 360
Db 301 NHPKNLFAAISTROYNNNLPITYSGRESNVQKMAISELMADVGISVDMDYGPSGSGS 360
QY 361 SRVORALKENFGYNQSVHQINRSDQDWEAQIDKELSONQPVYQGGKVGGAHFVIDGA 420
Db 361 SRVORALKENFGYNQSVHQINRSDQDWEAQIDKELSONQPVYQGGKVGGAHFVIDGA 420
QY 421 DGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
Db 421 DGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468

RESULT 2
AAE37684
ID AAE37684 standard; protein; 468 AA.
XX
AC AAE37684;
XX
DT 06-OCT-2003 (first entry)
XX
DE Streptococcus pyogenes SpEA-SpeB fusion protein.

```

```

XX Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpEA;
KW gene therapy; fusion protein; SpeB.
XX
OS Streptococcus pyogenes.
PN WO2003056015-A1.
PD 10-JUL-2003.
XX
PF 26-NOV-2001; 2001WO-US046540.
XX
PR 26-NOV-2001; 2001US-00002784.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Ulrich RG;
XX
WPI; 2003-492125/46.
DR N-PSDB; AAD56778.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
PS Claim 10; Page 134; 141pp; English.
XX
CC The invention provides a superantigen toxin DNA fragment which has been
CC genetically altered such that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is disrupted or
CC altered. DNA fragments of the invention are useful in the production of
CC vaccines against bacterial superantigen toxin infections. They are also
CC useful in gene therapy. The present sequence is Streptococcus pyogenes
CC pyrogenic exotoxin A (SpEA)-SpeB fusion protein. This sequence is used in
CC the invention
XX
SQ Sequence 468 AA;
Query Match 100.0%; Score 2500; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 6.9e-195;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
Db 1 MQQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
QY 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLPIPKIVVK 120
Db 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLPIPKIVVK 120
QY 121 VSIDGQISLSPDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQISLSPDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDLSKGIHYNQGNP 240
Db 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDLSKGIHYNQGNP 240
QY 241 YNLLTPVIEKVPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
Db 241 YNLLTPVIEKVPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
QY 301 NHPKNLFAAISTROYNNNLPITYSGRESNVQKMAISELMADVGISVDMDYGPSGSGS 360
Db 301 NHPKNLFAAISTROYNNNLPITYSGRESNVQKMAISELMADVGISVDMDYGPSGSGS 360
QY 361 SRVORALKENFGYNQSVHQINRSDQDWEAQIDKELSONQPVYQGGKVGGAHFVIDGA 420
Db 361 SRVORALKENFGYNQSVHQINRSDQDWEAQIDKELSONQPVYQGGKVGGAHFVIDGA 420
QY 421 DGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
Db 421 DGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:47:53 ; Search time 152.962 Seconds
(without alignments)
1183.322 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDPDPSSLHRSLLVKNLQ.....ALGTGGGAGFNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2500	100.0	468	7 ABU62335	ABU62335 SPEa L42R
2	2500	100.0	468	7 AAE37684	Aae37684 Streptoco
3	2484	99.4	468	7 AAE37691	Aae37691 S. pyogen
4	1332	53.3	248	7 ABU62333	ABU62333 Streptoco
5	1332	53.3	248	7 AAE37686	Aae37686 Streptoco
6	1327.5	53.1	398	2 AAU07898	AAU07898 Streptoco
7	1327.5	53.1	398	2 AAR95856	Aar95856 S. pyogen
8	1327.5	53.1	398	2 AAY81812	Aay81812 S. pyogen
9	1327.5	53.1	398	8 ADP89840	ADP89840 Streptoco
10	1324.5	53.0	398	7 ABU62332	ABU62332 Streptoco
11	1323.5	52.9	398	5 ABP29579	ABP29579 Streptoco
12	1323.5	52.9	398	7 AAE37685	Aae37685 Streptoco
13	1323.5	52.9	398	8 ADR83971	ADR83971 S. pyogen
14	1322	52.9	248	7 AAE37690	Aae37690 S. pyogen
15	1195.5	47.8	398	3 AAB36098	AAB36098 Streptoco
16	1168	46.7	220	7 ABU62334	ABU62334 Streptoco
17	1168	46.7	220	7 AAE37687	Aae37687 Streptoco
18	1163	46.5	220	7 AAE37689	Aae37689 S. pyogen
19	1162	46.5	220	7 AAE37688	Aae37688 S. pyogen
20	1136	45.4	251	3 AAY70109	Aay70109 Streptoco
21	1136	45.4	251	5 ABB79508	Abb79508 Streptoco
22	1136	45.4	251	6 ABU10088	Abu10088 Streptoco
23	1136	45.4	251	7 ABU62331	ABU62331 Streptoco
24	1136	45.4	251	7 AAE37683	Aae37683 Streptoco
25	1130	45.2	251	7 ABU62460	ABU62460 Streptoco

26	1129	45.2	221	4 AAB67344	Aab67344 Streptoco
27	1129	45.2	251	8 ADR89839	Adr89839 Streptoco
28	1123	44.9	221	2 AAR13209	Aar13209 Streptoco
29	1123	44.9	221	2 AAR45017	Aar45017 Staphyloc
30	1123	44.9	221	5 ABB76240	Abb76240 Staphyloc
31	1122	44.9	251	2 AAW12097	Aaw12097 Streptoco
32	1122	44.9	251	2 AAW59780	Aaw59780 Amino aci
33	1119	44.8	251	2 AAW12154	Aaw12154 Streptoco
34	1118	44.7	251	2 AAW12146	Aaw12146 Streptoco
35	1117.5	44.7	250	2 AAW12145	Aaw12145 Streptoco
36	1117	44.7	251	2 AAW12150	Aaw12150 Streptoco
37	1117	44.7	251	2 AAW12147	Aaw12147 Streptoco
38	1113	44.5	251	2 AAW12148	Aaw12148 Streptoco
39	1112	44.5	251	2 AAW12153	Aaw12153 Streptoco
40	1112	44.5	251	2 AAW12151	Aaw12151 Streptoco
41	1112	44.5	251	2 AAW12152	Aaw12152 Streptoco
42	1107	44.3	251	2 AAW12149	Aaw12149 Streptoco
43	1107	44.3	251	2 AAW59798	Aaw59798 Amino aci
44	1107	44.3	251	2 AAW59781	Aaw59781 Amino aci
45	938.5	37.5	250	6 ABU79074	Abu79074 S. pyogen

ALIGNMENTS

RESULT 1
ABU62335
ID ABU62335 standard; protein; 468 AA.
XX
AC ABU62335;
XX
DT 27-AUG-2003 (first entry)
XX
DE SPEa L42R/SPEb C47S mutant fusion protein.
XX
KW SPEa; streptococcus pyrogenic enterotoxin; mutant; vaccine; mutein;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial; SPEb.
XX
OS Streptococcus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 43 /label= Wild-type Leu substituted by Arg
FT Misc-difference 100..101 /note= "Encoded by ATCTACGGA"
FT Misc-difference 211..212 /note= "Encoded by ACNAGCCAA"
FT Misc-difference 386..387 /note= "Encoded by AGCAACAAA"
FT Misc-difference 407..408 /note= "Encoded by GGTGTGGGT"
US2003036644-A1.
20-FEB-2003.
26-NOV-2001; 2001US-00002784.
25-JUN-1997; 97US-00882431.
01-SEP-1998; 98US-00144776.
(ULRI/) ULRICH R G.
Ulrich RG;
WPI; 2003-492125/46.
N-PSDB; ACD28908.
New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Charles H. Harris
;; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
;; CITY: FORT DETRICK
;; STATE: MARYLAND
;; COUNTRY: USA
;; ZIP: 21702-5012
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.5
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/882,431B
;; FILING DATE: June 25, 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Charles H. Harris
;; REGISTRATION NUMBER: 34,616
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 619-2065
;; TELEFAX: (301) 619-7714
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 266
;; TYPE: Amino Acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;; US-08-882-431B-6

Query Match 42.9%; Score 567.5; DB 4; Length 266;
Best Local Similarity 47.5%; Pred. No. 1.9e-46;
Matches 121; Conservative 40; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS-QEVEFA--QQDDPDSQLHSSSLVKNL-QNIYFLEYEGDPVTHENVKSVQDQ 70
Db 11 ILIFALILVISTPNVLAESQDPDPDELHKSKFTGLMEDMKVLYDDNHVSAINVKSIDQ 70

QY 71 LRSHDLIYNVSGP---NYDKLTKELKNQEMATLFDKNVDIYGVVYHLCYCENA---- 123
Db 71 FLYFDLIYSIKDTKLGDYDNVRVEFNKDLADKYKDYVDVFCGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTHNEGNHLEIPKKIVKVSIDGIQSLSPDIETNKQMTAQELDYK 178
Db 131 SHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFDGKNLLSFDVQTNKKKVTQAELDYL 190

QY 179 VRKYLTDNKOLYNGPSKYETGYIKTIPKNKESFWDFPPEP---EFTOSKYLMIYKDNET 236
Db 191 TRHYLVKNKKGLYFNNSPYETGYIKFT-ENENSFYWDMPAPGDKFAQSKYLLMMYNDNM 249

QY 237 LDSNTSOIEVYLTTK 251
Db 250 VDSKDVKIEVYLTTK 264

Search completed: September 17, 2005, 00:48:30
Job time : 14.9638 secs

THIS PAGE BLANK (USPTO)

QY 124 --ERSACIYGGVTHNHEGHNLEIPKKIVVKVSDIGTQSLSFDTETNKKMVTAEQELDYKVRK 181
Db 123 TDKRKTCTMYGGVTEHNGNQLDKYRSITVRVFDGKNLLSFDVQTNKKKVTAEQELDYLTRH 182
QY 182 YLTDNKKQLYTNGPSKYETGYIKFIPKNKESFWDFFPEP--EFTOSKYLMIYKDNETLDS 239
Db 183 YLVKVKKLYEFNNSPYETGYIKFI-ENENSFWDMMAPGDKFDQSKYKLMYNDNKNVDS 241
QY 240 NTSQIEVYLTTK 251
Db 242 KDVKIEVYLTTK 253

RESULT 13
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Arntzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match 43.5%; Score 575; DB 3; Length 266;
Best Local Similarity 47.2%; Pred. No. 3.5e-47;
Matches 125; Conservative 40; Mismatches 78; Indels 22; Gaps 8;
QY 8 LKXNVFF---VLVTFGLGLIIS-QEVFA--QQDDPSQLHRSSLVKNL-QNIYFLYEGDPV 60
Db 1 MDKRLFISHVILFALILVISTPNVLAESQDPKDELHKSKFTGLMENKVLXDNDHV 60
QY 61 THENKVSVDQLRSHDLIYNVSGP---NYDKLKTTELKQEMATLFXDKKNVDIYGVYHLC 117
Db 61 SAINVKSIDQSLYFDLIYSIKDTKLGNVDNRVFEFKNKOLADKYDKYVDVFGANYIYOC 120
QY 118 YLCENA-----ERSACIYGGVTHNHEGHNLEIPKKIVVKVSDIGTQSLSFDTETNKK 168
Db 121 YFSKKTNDINSHQTKRKTCTMYGGVTEHNGNQLDKYRSITVRVFDGKNLLSFDVQTNKK 180
QY 169 MYTAEQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKESFWDFFPEP--EFTQSK 226
Db 181 KVTAQELDYLTRHYLVKVKKLYEFNNSPYETGYIKFI-ENENSFWDMMAPGDKFDQSK 239
QY 227 YLMIYKDNETLDSNTSQIEVYLTTK 251
Db 240 YLMYNDNKNVDSKDVKIEVYLTTK 264

RESULT 14
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
ATTN: MCMR-JA (Charles H. Harris-Patent
City: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match 42.9%; Score 567.5; DB 3; Length 266;
Best Local Similarity 47.5%; Pred. No. 1.8e-46;
Matches 121; Conservative 40; Mismatches 75; Indels 19; Gaps 7;
QY 15 VLVTFLGLTIS-QEVFA--QQDDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSDVQ 70
Db 11 ILIFALILVISTPNVLAESQDPKDELHKSKFTGLMEDMKVLYDDNHVSAINVKSIDQ 70
QY 71 LRSHDLIYNVSGP---NYDKLKTTELKQEMATLFXDKKNVDIYGVYHLCYLCENA---- 123
Db 71 FLYPFLIYSIKDTKLGDYDNRVFEFKNKOLADKYDKYVDVFGANYIYQCYFSKKTNDIN 130
QY 124 -----ERSACIYGGVTHNHEGHNLEIPKKIVVKVSDIGTQSLSFDTETNKKMVTAEQELDYK 178
Db 131 SHQTKRKTCTMYGGVTEHNGNQLDKYRSITVRVFDGKNLLSFDVQTNKKKVTAEQELDY 190
QY 179 VRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKESFWDFFPEP--EFTOSKYLMIYKDNET 236
Db 191 TEHYLVKVKKLYEFNNSPYETGYIKFI-ENENSFWDMMAPGDKFDQSKYKLMYNDNKNV 249
QY 237 LDSNTSQIEVYLTTK 251
Db 250 VDSKDKVIEVYLTTK 264

RESULT 15
US-08-882-431B-6
; Sequence 6, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25

```
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-20

Query Match          74.1%; Score 979.5; DB 4; Length 220;
Best Local Similarity 86.7%; Pred. No. 3.7e-86;
Matches 189; Conservative 4; Mismatches 24; Indels 1; Gaps 1;

QY 34 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENKVSVDQLRSHDLIYVNSGPNYDKLTCLK 93
Db 4 PRESQQRSLNLTFFKIYIFFMRVTLVTHENKVSVDQLRSHDLIYVNSGPNYDKLTCLK 63

QY 94 NQEMATLFDKKNVDIYGVVEYHLCYLCENASACIYGGVTNHEGHNLEIPKKIVVKVSI 153
Db 64 NQEMATLFDKKNVDIYGVVEYHLCYLCENASACIYGGVTNHEGHNLEIPKKIVVKVSI 123

QY 154 DGIQSLSPDIETNKKMWTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 213
Db 124 DGIQSLSPDIETNKKMWTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 182

QY 214 FDFPPEPFTQSKYLMYKDNETLDSNTSQIEVLYTTK 251
Db 183 FDFPPEPFTQSKYLMYKDNETLDSNTSQIEVLYTTK 220

RESULT 11
US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-2

Query Match          44.5%; Score 588; DB 1; Length 255;
Best Local Similarity 47.2%; Pred. No. 1.9e-48;
Matches 119; Conservative 41; Mismatches 76; Indels 16; Gaps 5;

QY 15 VLVTFGLTISQEVFAQODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENKVSVDQLRS 73
Db 3 MITNLIRLTIGNSMESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLY 62

QY 74 HDLIYNVSGP---NYDKLKTTELKNOEMATLFDKKNVDIYGVVEYHLCYLCENA----- 123
Db 63 FDLIYSIKDTKLGNDYDNRVRFKNDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSQ 122

QY 124 --ERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQLSFDIETNKKMWTAQELDYKVRK 181
Db 123 TDKRKTVMYGGVTEHNGNQLDKYRSITVRVPEDEGKNLLSFDVQTNKKKVTAEQLDYLTRH 182

QY 182 YLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPPEP--EFTQSKYLMYKDNETLDS 239
Db 183 YLVKKNKLYEFNNSPYETGYIKFI-ENENSWFYDMMWPAFGDPQSKYLMYKDNNDNKQVDS 241

QY 240 NTSQIEVLYTTK 251
Db 242 KDVKEIVLYTTK 253

RESULT 12
US-08-580-806-2
; Sequence 2, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-2

Query Match          44.5%; Score 588; DB 2; Length 255;
Best Local Similarity 47.2%; Pred. No. 1.9e-48;
Matches 119; Conservative 41; Mismatches 76; Indels 16; Gaps 5;

QY 15 VLVTFGLTISQEVFAQODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENKVSVDQLRS 73
Db 3 MITNLIRLTIGNSMESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLY 62

QY 74 HDLIYNVSGP---NYDKLKTTELKNOEMATLFDKKNVDIYGVVEYHLCYLCENA----- 123
Db 63 FDLIYSIKDTKLGNDYDNRVRFKNDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSQ 122
```

```
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match      88.0%; Score 1163; DB 4; Length 221;
Best Local Similarity 99.1%; Pred. No. 8.7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 QDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90
Db 1 QDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 60

QY 91 ELKNQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 150
Db 61 ELKNQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120

QY 151 VSDIGTQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKE 210
Db 121 VSDIGTQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKE 180

QY 211 SFWFDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
Db 181 SFWFDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 8
US-08-896-933-20
; Sequence 20, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20

Query Match      74.1%; Score 979.5; DB 3; Length 220;
Best Local Similarity 86.7%; Pred. No. 3.7e-86;
Matches 189; Conservative 4; Mismatches 24; Indels 1; Gaps 1;

QY 34 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLTK 93
Db 4 PKPSQLQRSNLVTKFYIFFMRVTLVTHENVKSVQDLRSHDLIYVNSGPNYDKLTK 63

QY 94 NOEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVKVSI 153
Db 64 NOEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVKVSI 123

QY 154 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 213
Db 124 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 182

QY 214 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
Db 183 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 10
US-09-708-008B-20
; Sequence 20, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
```

```
QY 214 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
Db 183 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 9
US-09-314-235-20
; Sequence 20, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match      74.1%; Score 979.5; DB 3; Length 220;
Best Local Similarity 86.7%; Pred. No. 3.7e-86;
Matches 189; Conservative 4; Mismatches 24; Indels 1; Gaps 1;

QY 34 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLTK 93
Db 4 PKPSQLQRSNLVTKFYIFFMRVTLVTHENVKSVQDLRSHDLIYVNSGPNYDKLTK 63

QY 94 NOEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVKVSI 153
Db 64 NOEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVKVSI 123

QY 154 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 213
Db 124 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 182

QY 214 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
Db 183 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 10
US-09-708-008B-20
; Sequence 20, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
```

US-08-896-933-29
; Sequence 29, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29

Query Match 88.0%; Score 1164; DB 3; Length 221;
Best Local Similarity 99.1%; Pred. No. 7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 90
DB 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 60
QY 91 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 150
DB 61 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210
DB 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 181 SFWDFLPPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 5
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 88.0%; Score 1164; DB 3; Length 221;

Best Local Similarity 99.1%; Pred. No. 7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 90
DB 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 60
QY 91 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 150
DB 61 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210
DB 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 181 SFWDFLPPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 6
US-09-708-008B-29
; Sequence 29, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-29

Query Match 88.0%; Score 1164; DB 4; Length 221;
Best Local Similarity 99.1%; Pred. No. 7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 90
DB 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 60
QY 91 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 150
DB 61 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210
DB 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 181 SFWDFLPPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 7
US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Steehr, Jennifer
; APPLICANT: Ohlendorf, Douglas

Best Local Similarity 100.0%; Pred. No. 5.6e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNKKVLKQWFFVFLVTLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKQWFFVFLVTLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKNVDIYGVYYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKNVDIYGVYYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSPDIETNKKMVTAAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSPDIETNKKMVTAAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 2
US-08-882-431B-16
; Sequence 16, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MWC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-16

Query Match 100.0%; Score 1322; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.6e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNKKVLKQWFFVFLVTLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKQWFFVFLVTLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKNVDIYGVYYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKNVDIYGVYYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSPDIETNKKMVTAAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSPDIETNKKMVTAAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 3
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USNO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PPT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-13

Query Match 98.9%; Score 1308; DB 4; Length 251;
Best Local Similarity 99.2%; Pred. No. 1.2e-117;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNNKKVLKQWFFVFLVTLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKQWFFVFLVTLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKNVDIYGVYYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKNVDIYGVYYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSPDIETNKKMVTAAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSPDIETNKKMVTAAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 4

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:42:17 ; Search time 13.9638 Seconds
(without alignments)
1341.817 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322

Sequence: 1 MNNKKVLKMMVFFVLVTFL.....KDNETLDSNTSQIEVLTITK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfileseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1322	100.0	251	3	US-09-144-776B-16
2	1322	100.0	251	4	US-08-882-431B-16
3	1308	98.9	251	4	US-08-973-391C-13
4	1164	88.0	221	3	US-08-896-933-29
5	1164	88.0	221	3	US-09-314-235-29
6	1164	88.0	221	4	US-09-708-008B-29
7	1163	88.0	221	4	US-08-973-391C-14
8	979.5	74.1	220	3	US-08-896-933-20
9	979.5	74.1	220	3	US-09-314-235-20
10	979.5	74.1	220	4	US-09-708-008B-20
11	588	44.5	255	1	US-08-446-918A-2
12	588	44.5	255	2	US-08-580-806-2
13	575	43.5	266	3	US-09-414-276-8
14	567.5	42.9	266	3	US-09-144-776B-6
15	567.5	42.9	266	4	US-08-882-431B-6
16	563	42.6	239	3	US-09-144-776B-10
17	563	42.6	239	4	US-08-882-431B-10
18	561	42.4	239	3	US-08-896-933-26
19	561	42.4	239	3	US-09-314-235-26
20	561	42.4	239	4	US-09-708-008B-26
21	558.5	42.2	266	3	US-09-144-776B-8
22	558.5	42.2	266	4	US-08-882-431B-8
23	553	41.8	266	3	US-09-144-776B-14
24	553	41.8	266	4	US-08-882-431B-14
25	545	41.2	238	3	US-08-896-933-28
26	545	41.2	238	3	US-09-314-235-28
27	545	41.2	238	4	US-09-708-008B-28

28	544	41.1	239	3	US-08-896-933-27	Sequence 27, Appl
29	544	41.1	239	3	US-09-314-235-27	Sequence 27, Appl
30	544	41.1	239	4	US-09-708-008B-27	Sequence 27, Appl
31	522	39.5	239	3	US-08-896-933-21	Sequence 21, Appl
32	522	39.5	239	3	US-09-314-235-21	Sequence 21, Appl
33	522	39.5	239	4	US-09-708-008B-21	Sequence 21, Appl
34	424	32.1	79	3	US-09-144-776B-24	Sequence 24, Appl
35	424	32.1	79	4	US-08-882-431B-24	Sequence 24, Appl
36	328.5	24.8	228	3	US-08-896-933-25	Sequence 25, Appl
37	328.5	24.8	228	4	US-09-314-235-25	Sequence 25, Appl
38	328.5	24.8	228	4	US-09-708-008B-25	Sequence 25, Appl
39	308	23.3	257	3	US-08-486-099-112	Sequence 112, App
40	308	23.3	257	3	US-08-360-107A-122	Sequence 122, App
41	308	23.3	257	3	US-08-484-223B-112	Sequence 112, App
42	308	23.3	257	3	US-08-919-597-112	Sequence 112, App
43	308	23.3	257	3	US-08-475-668A-112	Sequence 112, App
44	308	23.3	257	3	US-08-485-551A-112	Sequence 112, App
45	308	23.3	257	3	US-08-471-913A-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16
Query Match 100.0% Score 1322; DB 3; Length 251;


```
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Direct protein sequencing; Enterotoxin; Signal;
KW Supranatigen; Toxin.
FT SIGNAL 1 27
FT CHAIN 28 266 Enterotoxin type B.
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
FT STRAND 29 29
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 52
FT HELIX 53 55
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 83 85
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 108 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 127 128
FT STRAND 138 142
FT STRAND 145 147
FT TURN 149 150
FT STRAND 152 165
FT TURN 166 167
FT STRAND 168 179
FT STRAND 181 183
FT HELIX 184 199
FT STRAND 209 218
FT TURN 219 220
FT STRAND 221 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 255 263
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;

Query Match 43.6%; Score 576.5; DB 1; Length 266;
Best Local Similarity 48.2%; Pred. No. 4.4e-35;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS--QDDPDPQLHRSSLVKML-QNIYFLYSGDPVTHENVKSV 70
DB 11 ILIFALLIVSTPNVLAESQDPDPDELHKSKFTGLMENMKVLYDDNHVSAINVKSIDQ 70

QY 71 LRSHDLIYNVSGP---PNYDKLTKEKNQEMATLFDKNVDIYGVYHLCYLCEA----123
DB 71 FLYFDLIYSIKDTKLGNDYDNRVFEKNGKOLADKYDKYDVFNGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTHNHEGNHLEIPKIVVKVSIIDGIQSLSPDIETNKKMVTQAQLDYK 178

DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Direct protein sequencing; Enterotoxin; Signal;
KW Supranatigen; Toxin.
FT SIGNAL 1 27
FT CHAIN 28 266 Enterotoxin type B.
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
FT STRAND 29 29
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 52
FT HELIX 53 55
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 83 85
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 108 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 127 128
FT STRAND 138 142
FT STRAND 145 147
FT TURN 149 150
FT STRAND 152 165
FT TURN 166 167
FT STRAND 168 179
FT STRAND 181 183
FT HELIX 184 199
FT STRAND 209 218
FT TURN 219 220
FT STRAND 221 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 255 263
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;

Query Match 43.6%; Score 576.5; DB 1; Length 266;
Best Local Similarity 48.2%; Pred. No. 4.4e-35;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS--QDDPDPQLHRSSLVKML-QNIYFLYSGDPVTHENVKSV 70
DB 11 ILIFALLIVSTPNVLAESQDPDPDELHKSKFTGLMENMKVLYDDNHVSAINVKSIDQ 70

QY 71 LRSHDLIYNVSGP---PNYDKLTKEKNQEMATLFDKNVDIYGVYHLCYLCEA----123
DB 71 FLYFDLIYSIKDTKLGNDYDNRVFEKNGKOLADKYDKYDVFNGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTHNHEGNHLEIPKIVVKVSIIDGIQSLSPDIETNKKMVTQAQLDYK 178
```

```
Db 131 SHQTDKRTKTYGGVTEHNGQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTQAQLDY 190
QY 179 VRKYLTDNKLQYTNQPSKYETGYIKFIPKNKESFWDFPFPEP--EFTQSKYLMYKDNET 236
Db 191 TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSEFWYDMMAPAGDKFDQSKYLMWYNDNM 249
QY 237 LDSNTSQIEVVLTTK 251
Db 250 VDSKDVKIEVVLTTK 264

RESULT 13
Q9F0L6 PRELIMINARY; PRT; 271 AA.
AC Q9F0L6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcal enterotoxin C-bovine.
GN Name=sec-Bov;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=11114901; DOI=10.1128/JB.183.1.63-70.2001;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70(2001).
DR EMBL; AF217235; AAG29599.1; -.
DR HSSP; P34071; I14X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrj_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493FG228B042F10 CRC64;

Query Match 42.0%; Score 555; DB 2; Length 271;
Best Local Similarity 44.9%; Pred. No. 1.8e-33;
Matches 115; Conservative 51; Mismatches 72; Indels 18; Gaps 8;

QY 11 MVF-FVLVTFLGLTISQEVFAQQDDPDPQLHRSSLVKML-QNIYFLYSGDPVTHENVKSV 68
Db 17 LIFALLIVLFTPNVLAES--SQDDPDPDELHKSKFTGLMENMKVLYDDRYVSATKXSV 73

QY 69 DQLRSHDLIYNVSG---PNYDKLTKEKNQEMATLFDKNVDIYGVYHLCYLCEA--ENA 123
Db 74 DKFLAHDLIYNISDKKLNKYDKVKTTELLNEDLAKYKDEVDVYGSNTYVNCYFSSKNV 133

QY 124 ER---SACIYGGVTHNHEGNHLEIPK--KIVVKVSIIDGIQSLSPDIETNKKMVTQAQLDY 177
Db 134 KGVYGGKTCMGGITKHEGNHFDNGLQNVLIRVYENKNTISFVQDKSKVTAQLDI 193

QY 178 KVRKYLTDNKLQYTNQPSKYETGYIKFIPKNKESFWDFPFPEP--EFTQSKYLMYKONE 235
Db 194 KARNFLINKNLYEFNNSPYETGYIKFIENNGTWFYDMMAPAGDKFDQSKYLMWYNDNM 253
QY 236 LDSNTSQIEVVLTTK 251
Db 254 TVDSKSVKIEVHLTTK 269
```

```

OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D633;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izso M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF029051; AAD21315.1; -.
DR HSSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 8.4e-71;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 21 GLTISVEFAQQDPDSQLRSSLVKNLQNIYFLYEGDPVTHENVKSVLDQLSHDLIYV 80
DB 1 GLTTSVEFAQQDPNSQLRSSLVKNLQNIYFLYEGDPVTHENVKSVLDQLSHDLIYV 60

QY 81 SGNPYDKLTAKNQEMATLFDKNVDIYGVYHYH.CYLCENASRACIYGGVTNHEGNH 140
DB 61 SGLNYDKLTAKNREMSLTFKNKNVDIYGVYHYH.CYLCENAKRACIYGGVTNHEGNH 120

QY 141 LEIPKVIKVSIDGTSQSLFSDIETKKNVTAQELDYKVRKYLTDNKLQIYTGSPSKYETG 200
DB 121 LEIPKVIKVSIDGTSQSLFSDIETSKKNVTAQELDYKVRKYLTDNKLQIYTGSPSKYETG 180

QY 201 YIKFIPKNKESWFDFPFPEFTOSKYLMIYKDNETLDSNTS 242
DB 181 YIKFISKDXTFWDFPFPEFQVQVLYMIYKDNETLDSSTS 222

RESULT 12
ETXB STAAU
ID ETXB STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Enterotoxin type B precursor (SEB).
GN Name:entB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus.";
RL J. Bacteriol. 166:29-33(1986).
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.

RX MEDLINE=85298255; PubMed=3898073;
RA Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia
RT coli and Staphylococcus aureus.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN [3]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin B,
RT and the complete amino acid sequence.";
RL J. Biol. Chem. 245:3518-3525(1970).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0;
RA Swaminathan S., Furey W.P. Jr., Pletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RL Nature 359:801-806(1992).
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
RA Jardtetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RA Chi Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RL Nature 368:711-718(1994).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=99096298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80646-9;
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
RA Karjalainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN [7]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M1118; AAA88550.1; -.
DR FIR; S27360; ENSAB6.
DR PDB; 1D5M; X-ray; C=28-266.
DR PDB; 1D5X; X-ray; C=28-266.
DR PDB; 1D5Z; X-ray; C=28-266.
DR PDB; 1D6E; X-ray; C=28-266.
DR PDB; 1SBB; X-ray; B/D=28-266.
DR PDB; 1SE3; X-ray; @=28-266.
DR PDB; 1SE4; X-ray; @=28-266.
DR PDB; 1SEB; X-ray; D/H=29-262.
DR PDB; 2SEB; X-ray; D=28-266.
DR PDB; 3SEB; X-ray; @=28-266.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.

```

```

Qy 69 DQLRSHDLIYVSGPNYDKLTKEKLNQEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 128
Db 61 DQLLSDHDLIYVSGPNYDKLTKEKLNQEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 120

Qy 129 IYGGVTNHEGNHLEIPKVIWKVSDIGIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 188
Db 121 IYGGVTNHEGNHLEIPKVIWKVSDIGIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 180

Qy 189 LYTGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYL 228
Db 181 LYTGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYL 220

RESULT 9
ID Q54696 PRELIMINARY; PRT; 236 AA.
AC Q54696;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL, X61573; CAA43771.1; -.
DR F1R; S18789; S18789.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL 1 1
FT CHAIN <1 22 Potential.
FT NON_TER 23 >236 type A exotoxin.
FT SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 83.9%; Score 1109; DB 2; Length 236;
Best Local Similarity 88.6%; Pred. No. 7.1e-75;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 9 KKMVFVLVFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKIIVFLAIFGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

Qy 69 DQLRSHDLIYVSGPNYDKLTKEKLNQEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 128
Db 61 DQLLSDHDLIYVSGPNYDKLTKEKLNQEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 120

Qy 129 IYGGVTNHEGNHLEIPKVIWKVSDIGIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 188
Db 121 IYGGVTNHEGNHLEIPKVIWKVSDIGIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 180

```

```

Qy 189 LYTGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNLTDSNTSQI 244
Db 181 LYTGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNLTDSNTSQI 236

RESULT 10
Q538P4 PRELIMINARY; PRT; 222 AA.
ID Q538P4;
AC Q538P4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22508029; PubMed=12620634;
RA Kalia A., Bessen D.E.;
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT isolates of group G streptococci.";
RL FEMS Microbiol. Lett. 219:291-295 (2003).
DR EMBL; AY049745; AAL06068.1; -.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
FT SEQUENCE 222 AA; 25984 MW; 121F8460992818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 8.4e-71;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 21 GLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYV 80
Db 1 GLTTSQEVFAQQDDPNPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYV 60

Qy 81 SGPVYDKLTKEKLNQEMATLFKDKNVDIYGVYVHLCYLCEAERSACIYGVVTHNEGNH 140
Db 61 SGLNYDKLTKEKLNQEMATLFKDKNVDIYGVYVHLCYLCEAERSACIYGVVTHNEGNH 120

Qy 141 LEIPKKIYVVKVSDIGIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKKLYTGPSKYETG 200
Db 121 LEIPKNILVVKVSDIGIQSLSFDIETSKMVTQAQLDYKVRKHLTDNNQLYTGPSKYETG 180

Qy 201 YIKFIPKNKESFWDFPPEFTQSKYLMYKDNLTDSNTS 242
Db 181 YIKFISKDKETFWDFPPEFTQSKYLMYKDNLTDSSTS 222

RESULT 11
Q555Z4 PRELIMINARY; PRT; 222 AA.
ID Q555Z4;
AC Q555Z4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Exotoxin type A (Fragment).
GN Name=speA;

```

```
DR InterPro: IPR0061173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1 Potential.
FT SIGNAL <1 22 type A exotoxin.
FT CHAIN 23 >236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; 2EF7F41AACB53600 CRC64;

Query Match 93.3%; Score 1234; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 3.4e-84;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVSGPNYDKLTCLKNQEMATLFDKNVDIYGVVEYHLCYLCENASERSAC 128
Db 61 DQLRSHDLIYVSGPNYDKLTCLKNQEMATLFDKNVDIYGVVEYHLCYLCENASERSAC 120

QY 129 IYGVVTHHGNHLEIPKKIIVKVSIDGIQSLSPDIETNKKMVTAAQELDYKVRKYLTDNKQ 188
Db 121 IYGVVTHHGNHLEIPKKIIVKVSIDGIQSLSPDIETNKKMVTAAQELDYKVRKYLTDNKQ 180

QY 189 LYTNGPSKYETGVIKIPKNKESFWDFPPEPTQSKYLMYKDNETLDSNTSQI 244
Db 181 LYTNGPSKYETGVIKIPKNKESFWDFPPEPTQSKYLMYKDNETLDSNTSQI 236

RESULT 7
Q9R931 PRELIMINARY; PRT; 222 AA.
AC Q9R931;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D709;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF055698; AAD11624.1; -.
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006136; Staph/Strep_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
```

```
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 88.7%; Score 1173; DB 2; Length 222;
Best Local Similarity 99.5%; Pred. No. 1.1e-79;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 GLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV DQLRSHDLIYV 80
Db 1 GLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV DQLRSHDLIYV 60

QY 81 SGPNYDKLTCLKNQEMATLFDKNVDIYGVVEYHLCYLCENASERSACIYGVVTHHGNH 140
Db 61 SGPNYDKLTCLKNQEMATLFDKNVDIYGVVEYHLCYLCENASERSACIYGVVTHHGNH 120

QY 141 LEIPKKIIVKVSIDGIQSLSPDIETNKKMVTAAQELDYKVRKYLTDNKQIYTNGPSKYETG 200
Db 121 LEIPKKIIVKVSIDGIQSLSPDIETNKKMVTAAQELDYKVRKYLTDNKQIYTNGPSKYETG 180

QY 201 YIKFIPKNKESFWDFPPEPTQSKYLMYKDNETLDSNTS 242
Db 181 YIKFIPKNKESFWDFPPEPTQSKYLMYKDNETLDSNTS 222

RESULT 8
Q9A9Q0 PRELIMINARY; PRT; 220 AA.
AC Q9A9Q0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS500;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61554; CAA43752.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1 Potential.
FT SIGNAL <1 22 type A exotoxin.
FT CHAIN 23 >220
FT NON_TER 220 220
SQ SEQUENCE 220 AA; 25600 MW; 92DB096E57906DF6 CRC64;

Query Match 87.7%; Score 1159; DB 2; Length 220;
Best Local Similarity 99.5%; Pred. No. 1.2e-78;
Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60
```

```

DR GO:0009405; P: pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1 Potential.
FT SIGNAL <1 22 type A exotoxin.
FT CHAIN 23 >236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 93.8%; Score 1240; DB 2; Length 236;
Best Local Similarity 99.6%; Pred. No. 1.2e-84;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKMVFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKMVFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 128
Db 61 DQLLSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 120

QY 129 IYGVVTHNEGNHLEIPKKIIVKVSIDIGISLSDIETNKKMVTAGLDYKVRKYLTDNKK 188
Db 121 IYGVVTHNEGNHLEIPKKIIVKVSIDIGISLSDIETNKKMVTAGLDYKVRKYLTDNKK 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 244
Db 181 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 5
Q54779 PRELIMINARY; PRT; 236 AA.
AC Q54779; Q54613; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS485, MGAS158, MGAS491, MGAS495, and MGAS624;
RC MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61569; CAA43767.1; -
DR EMBL; X61568; CAA43766.1; -
DR EMBL; X61570; CAA43768.1; -
DR EMBL; X61571; CAA43769.1; -
DR EMBL; X61572; CAA43770.1; -
DR PIR; A60108; A60108.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P: pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.

```

```

DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1 Potential.
FT SIGNAL <1 22 type A exotoxin.
FT CHAIN 23 >236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 93.7%; Score 1239; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 1.4e-84;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKMVFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKMVFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 128
Db 61 DQLLSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 120

QY 129 IYGVVTHNEGNHLEIPKKIIVKVSIDIGISLSDIETNKKMVTAGLDYKVRKYLTDNKK 188
Db 121 IYGVVTHNEGNHLEIPKKIIVKVSIDIGISLSDIETNKKMVTAGLDYKVRKYLTDNKK 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 244
Db 181 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 6
Q57453 PRELIMINARY; PRT; 236 AA.
AC Q57453
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156, MGAS250, MGAS256, MGAS285, MGAS480, MGAS492, and MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61562; CAA43760.1; -
DR EMBL; X61561; CAA43759.1; -
DR EMBL; X61563; CAA43761.1; -
DR EMBL; X61564; CAA43762.1; -
DR EMBL; X61565; CAA43763.1; -
DR EMBL; X61566; CAA43764.1; -
DR EMBL; X61567; CAA43765.1; -
DR PIR; A60108; A60108.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P: pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.

```

FT STRAND 197 205
 FT STRAND 212 215
 FT HELIX 224 227
 FT HELIX 228 231
 FT TURN 232 233
 FT STRAND 236 238
 FT TURN 239 241
 FT STRAND 243 251
 SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCBFC3 CRC64;

Query Match 99.5%; Score 1315; DB 1; Length 251;
 Best Local Similarity 99.6%; Pred. No. 3.3e-90;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
 |||||
 Db 1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
 |||||

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFDKKNVDIYGVYHYHLCYL 120
 |||||
 Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFDKKNVDIYGVYHYHLCYL 120
 |||||

QY 121 ENAERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180
 |||||
 Db 121 ENAERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180
 |||||

QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240
 |||||
 Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240
 |||||

QY 241 TSQIEVYLTTK 251
 |||||
 Db 241 TSQIEVYLTTK 251
 |||||

RESULT 3

Q8K6K5
 ID Q8K6K5 PRELIMINARY; PRT; 251 AA.
 AC Q8K6K5; Q79XZ6;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Exotoxin type A-phage associated (SpeA precursor).
 GN Name=speA3; OrderedLocuNames=SP0560, SPYJ_1301;
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=198466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
 RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSI-1;
 RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
 RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
 RA Okabeashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
 RA Hayashi H., Hattori M., Hamada S.;
 RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
 RT large-scale genomic rearrangement in invasive strains and new insights
 RT into phage evolution.";
 RL Genome Res. 13:1042-1055(2003).
 DR EMBL; AE014161; AAM79908.1; -;
 DR EMBL; AF005142; BAC63655.1; -;

DR PIR; A60108; A60108.
 DR HSSP; P01552; 1SEB.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR Pfam; PF01123; Staph_strp_toxin; 1.
 DR Pfam; PF02876; Staph_strp_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN-
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCDS CRC64;

Query Match 99.4%; Score 1314; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 3.9e-90;
 Matches 249; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
 |||||
 Db 1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
 |||||

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFDKKNVDIYGVYHYHLCYL 120
 |||||
 Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFDKKNVDIYGVYHYHLCYL 120
 |||||

QY 121 ENAERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180
 |||||
 Db 121 ENAERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180
 |||||

QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240
 |||||
 Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240
 |||||

QY 241 TSQIEVYLTTK 251
 |||||
 Db 241 TSQIEVYLTTK 251
 |||||

RESULT 4
 P97163
 ID P97163 PRELIMINARY; PRT; 236 AA.
 AC P97163; P97164;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Type A exotoxin precursor (fragment).
 GN Name=speA;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS165; MGAS327; MGAS493; MGAS494; MGAS167; and MGAS156;
 RX MEDLINE=92044323; PubMed=1940804;
 RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RT "Characterization and clonal distribution of four alleles of the speA
 RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
 RT Streptococcus pyogenes.";
 RL J. Exp. Med. 174:1271-1274(1991).
 DR EMBL; X61556; CAA43754.1; -;
 DR EMBL; X61555; CAA43753.1; -;
 DR EMBL; X61557; CAA43755.1; -;
 DR EMBL; X61558; CAA43756.1; -;
 DR EMBL; X61559; CAA43757.1; -;
 DR EMBL; X61560; CAA43758.1; -;
 DR PIR; A60108; A60108.
 DR HSSP; P01552; 1SEB.
 DR GO; GO:0005576; C:extracellular; IEA.


```
KW Complete proteome; Signal; Toxin.
FT SIGNAL 1 30 By similarity.
FT CHAIN 31 251 Exotoxin type A.
FT DISULFID 117 128 By similarity.
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCBFCC3 CRC64;

Query Match 99.5%; Score 1315; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.3e-90;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNKKVLKVMFFVFLVTLTGITISQEVFAQDDPPSQRHRSVLKVLNQLNIYFLYEGDPV 60
Db 1 MENNKKVLKVMFFVFLVTLTGITISQEVFAQDDPPSQRHRSVLKVLNQLNIYFLYEGDPV 60

QY 61 THENYKSVQDLRSHDLIYNVSGPNVDKLTTELKNOEMATLFDKKNVDIYGVVYHLCYL 120
Db 61 THENYKSVQDLRSHDLIYNVSGPNVDKLTTELKNOEMATLFDKKNVDIYGVVYHLCYL 120

QY 121 ENAERSACIYGGVTHNEGHNHLEIPKIVVKVSDIGIQSLSDIETNKKMVTAAQELDYKVR 180
Db 121 ENAERSACIYGGVTHNEGHNHLEIPKIVVKVSDIGIQSLSDIETNKKMVTAAQELDYKVR 180

QY 181 KYLTNKKQLYNTGSPSKYETGIKFIKPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
Db 181 KYLTNKKQLYNTGSPSKYETGIKFIKPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTK 251
Db 241 TSQIEVYLTK 251

RESULT 2
SPEA_STRPY STANDARD; PRT; 251 AA.
AC P62560; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_taxid=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12."
RL Infect. Immun. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italian J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT receptors."
RL EMBO J. 18:9-21(1999).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.
CC
```

CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta chain.

CC -!- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12.

CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC

CC EMBL; U00453; AAC48868.1; -.

CC EMBL; X03929; CAA27568.1; -.

CC PIR; A26152; A26152.

CC PDB; 1B1Z; X-ray; -.

CC PDB; 1FNU; X-ray; -.

CC PDB; 1FNV; X-ray; -.

CC PDB; 1FNW; X-ray; -.

CC PDB; 1HA5; X-ray; -.

CC PDB; 1LOX; X-ray; -.

CC InterPro; IPR008992; Bact_endotox.

CC InterPro; IPR006177; Bctrl_tox.

CC InterPro; IPR006123; Staph/Strep_toxin.

CC InterPro; IPR006126; Staph/Strep_tox.

CC InterPro; IPR006173; Staph_tox_OB.

CC Pfam; PF02876; Staph_strep_tox_C; 1.

CC Pfam; PF01123; Staph_strep_toxin; 1.

CC PRINTS; PR00279; BACTRLTOXIN.

CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

CC 3D-structure; Signal; toxin.

FW SIGNAL 1 30

FT CHAIN 31 251 Exotoxin type A.

FT DISULFID 117 128

FT CONFLICT 6 6 K -> E (in Ref. 2).

FT CONFLICT 17 18 VT -> MK (in Ref. 2).

FT CONFLICT 25 35 SQEVAQQDDP -> LPKGICSTRPK (in Ref. 2).

FT CONFLICT 40 40 H -> Q (in Ref. 2).

FT CONFLICT 43 43 S -> N (in Ref. 2).

FT CONFLICT 47 59 NLQNIYFLYEGDP -> TFKIYIFPMRVTL (in Ref. 2).

FT CONFLICT 129 129 I -> L (in Ref. 2).

FT CONFLICT 165 178 TNKGWVTAQELDYK -> QIKNGNCSRISYT (in Ref. 2).

FT TURN 36 38

FT HELIX 42 44

FT TURN 46 48

FT HELIX 49 56

FT STRAND 60 65

FT STRAND 69 69

FT TURN 73 74

FT STRAND 75 78

FT STRAND 82 82

FT TURN 83 84

FT STRAND 85 85

FT STRAND 87 91

FT HELIX 95 102

FT TURN 103 103

FT STRAND 106 110

FT STRAND 113 113

FT TURN 115 116

FT TURN 121 122

FT STRAND 126 130

FT STRAND 133 135

FT TURN 137 138

FT STRAND 140 153

FT TURN 154 155

FT STRAND 156 167

FT STRAND 169 171

FT HELIX 172 186

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:48:38 ; Search time 79.5939 Seconds
(without alignments)
1614.846 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322

Sequence: 1 MENNKKVLKMWFFVLVTFLL.....KNETILDSNTSQIEVLLTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1315	99.5	251	1 SPEA_STRP8	P62561 streptococ
2	1315	99.5	251	1 SPEN_STRPY	P62560 streptococ
3	1314	99.4	251	2 Q8K6K5	Q8K6K5 streptococ
4	1240	93.8	236	2 P97163	P97163 streptococ
5	1239	93.7	236	2 Q54779	Q54779 streptococ
6	1234	93.3	236	2 Q57453	Q57453 streptococ
7	1173	88.7	222	2 Q98931	Q98931 streptococ
8	1159	87.7	220	2 Q79AQ0	Q79AQ0 streptococ
9	1109	83.9	236	2 Q54696	Q54696 streptococ
10	1054	79.7	222	2 Q938P4	Q938P4 streptococ
11	1054	79.7	222	2 Q985Z4	Q985Z4 streptococ
12	576.5	43.6	266	1 ETXB_STAAU	P01552 staphylococ
13	555	42.0	271	2 Q9F0L6	Q9F0L6 staphylococ
14	553	41.8	266	2 Q8XNJ6	Q8XNJ6 staphylococ
15	551.5	41.7	266	1 ETC3_STAAM	P23313 staphylococ
16	551	41.7	239	2 Q53678	Q53678 staphylococ
17	550	41.6	239	2 Q06532	Q06532 staphylococ
18	549	41.5	239	2 Q06533	Q06533 staphylococ
19	549	41.5	266	1 ETC2_STAAU	P34071 staphylococ
20	548	41.5	239	2 Q05157	Q05157 staphylococ
21	548	41.5	239	2 Q06531	Q06531 staphylococ
22	548	41.5	266	1 ETC1_STAAU	P01553 staphylococ
23	545	41.2	239	2 Q6ST49	Q6ST49 staphylococ
24	544	41.1	239	2 Q06535	Q06535 staphylococ
25	539	40.8	239	2 Q06534	Q06534 staphylococ
26	538	40.7	234	2 Q9R5X4	Q9R5X4 staphylococ
27	536.5	40.6	260	2 Q54971	Q54971 streptococ
28	531.5	40.2	260	2 Q54738	Q54738 streptococ
29	531.5	40.2	260	2 Q79X14	Q79X14 streptococ
30	531.5	40.2	260	2 Q54739	Q54739 streptococ
31	527	39.9	259	2 Q76LS8	Q76LS8 staphylococ

32	522	39.5	264	2	Q764P6	Q764P6 staphylococ
33	512.5	38.8	259	2	Q936G4	Q936G4 staphylococ
34	505	38.2	222	2	Q6XZE6	Q6XZE6 staphylococ
35	501	37.9	222	2	Q6XZE7	Q6XZE7 staphylococ
36	501	37.9	261	2	Q6XXM5	Q6XXM5 staphylococ
37	499	37.7	261	2	Q6YCN4	Q6YCN4 staphylococ
38	499	37.7	261	2	Q6GFN0	Q6GFN0 staphylococ
39	490	37.1	261	2	Q6XXM3	Q6XXM3 staphylococ
40	487	36.8	261	2	Q6XXM4	Q6XXM4 staphylococ
41	481	36.4	258	1	ETXG_STAAM	Q85382 staphylococ
42	472	35.7	258	2	Q6GFN2	Q6GFN2 staphylococ
43	471	35.6	258	2	Q9EZM3	Q9EZM3 staphylococ
44	471	35.6	258	2	Q9ZNF2	Q9ZNF2 staphylococ
45	470	35.6	214	2	Q6XZE8	Q6XZE8 staphylococ

ALIGNMENTS

RESULT 1

SPEA_STRP8
ID SPEA_STRP8 STANDARD; PRT; 251 AA.
AC P62561; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA; OrderedLocusNames=spyM18_0193;
OS Streptococcus pyogenes (serotype M18);
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RA "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
-!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever (By similarity).
CC
-!- SUBUNIT: Binds to major histocompatibility complex class II beta chain (By similarity).
-!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL; AE009982; AAL97141.1; -
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bctrl_tox.
InterPro; IPR006123; Staph/Strep_toxin.
InterPro; IPR006126; Staph/Strep_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF02876; Staph_strp_tox_C; 1.
Pfam; PF01123; Staph_strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

```
Best Local Similarity 34.1%, Pred. No. 1.2e-17;
Matches 91; Conservative 52; Mismatches 86; Indels 38; Gaps 13;

QY 10 KWVFFVLVTFLGLTI-----SQEVFAQDDPPSOLHRSSLVKNLQNIYELYEGD 58
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 5 KKTTFILLFIALTLITSPFVNCSEKSEEBEINGDLQKKSBLQGTAL--SNDRQYYI-HNGS 62
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 59 PVTHENVKSVQLRSHDLIYN--VSGPN-YDKLTELKNQEMATLFXDKKNVDIYGVVEYH 115
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 AII-ENKESNDQFLKNTILFNDFTHQWYNDLLVDLGSKDTANIYKGGKVDLYGVVY-- 119
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 116 LCVLCENAE--RSACIYGVVTHNHEGNHLEIPKIVKVSIDGIQSL--SPDIETNKKMWT 171
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 120 -GYQCTCGTFFKACMYGGVTHDNNQLEBEKKVPINLWDGKQNTVPLGTIVKTNKKEVT 178
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 172 AQELDYKVRKYLTDNKOLYT---NGPSKYETGVYKPKNKSFWDFPEPEFTQSKY 227
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 VQELDLQSRHYLHETNYLNTDAFNG--KIQRLGIEFHPSSGDSGVGYDLFG-----AQQY 232
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 228 ----LMIYKDNETLDSNTSQIEVYLT 250
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 233 PDTQLRIYRDNKTIKSKNMHDIYLYT 259
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
H89968
enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89968
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:Q9EZM4; GB:BA000018; PID:gl3701618; PIDN:BA042911.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: sen
C:Superfamily: enterotoxin B

Query Match 23.6%, Score 311.5; DB 2; Length 258;
Best Local Similarity 33.8%, Pred. No. 7.5e-16;
Matches 89; Conservative 49; Mismatches 102; Indels 23; Gaps 10;

QY 1 MNNKKVLKXWVFP---VLVTFGLTISQEVFAQDD---PDPSQLHRSSLVKNLQNIY- 52
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1 MKIYIKLMR--LFYIAIITLCLINNVTYNAEVDKOLKKSDDLSSKLF-NLTSYYT 57
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 53 -FLYEGDPVTHENVKSVQLRSHDLI---YNVSGPNYDKLTELKNQEMATLFXDKKNVDI 108
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 58 DITWQLD---ESNKKISTQLLNTIILKNIDISVLKTSLSKVEFNSSDLANQFKGNIDI 114
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 109 YGVEYHYLCY-LCENAEASACIYGVVTHNHEGNHLEIPKIVKVSIDGIQSLSFDIETNK 167
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 115 YGLYFGNKCVCGLTE--EKTSCLYGGVTHDGNQLDEEKVIGVNVFKDGVQOQEGFVTKTK 172
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 168 KMTAQELDYKVRKYLTDNKOLYTNPGSKYETGVYKIPKN--KESFWDFFPEPEFTQS 225
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 173 AKVTVQELDTKVRPKLENLYKNKDTGNTQKGCIFPHSHHQDQSPYDLYNVNKGVSVA 232
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 226 KYLMIYKDNETLDSNTSQIEVYL 248
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 233 EFPQFYSDNKTSSNNYHIDVFL 255
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: September 17, 2005, 01:14:33
Job time : 19.153 secs
```

THIS PAGE BLANK (USPTO)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33953
R;Bayles, K.W.; Tandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A;Reference number: A33953; MUID:99359112; PMID:2549000
A;Accession: A33953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <BAY>
A;Cross-references: UNIPROT:P20723; GE:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g7586595
C;Superfamily: enterotoxin B

Query Match	25.7%;	Score 340;	DB 2;	Length 258;
Best Local Similarity	35.2%;	Pred. No. 5.9e-102;		
Matches	92;	Conservative 47;	Mismatches 102;	Indels 20; Gaps 10
Qy	8	LKKM-VFPLVTFGLTISQ-EVFAQQDPD---PSQHR-----SSLVKNLQNIYFLYEG	57	
Db	1	MKFNILIALFTTSLVISPLNVKANENIDSVKEKELHKK3ELSLTALNNMKHSY--ADK	58	
Qy	58	DPVTHENVKVSVDLQRSHDLIYN--VSGPNVDKLTCLKNQSMATLFKDKNVDIYGVVEY	114	
Db	59	NPIIGENKSGDQFLNTELLYKPTDLINFDLLINFSKEMAQHFQSKNVDVVPIRXS	118	
Qy	115	HLCYLCENAESACTYGGVTHNGHLEIPKKIVVKVSTDGIQ-SLSFD-ETNKKMVT	172	
Db	119	INCYGGE-IDRTACTYGGVTHGNNKLERKKIPINLWINGVQKEVSLDKVOTDKNVT	177	
Qy	173	QELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKPKNESFWFFPEPEFTQSKYLM	230	
Db	178	QELDAQARYLQKDLKLYNNDTLGGKIQRGKTEFDSSDGSKVSYDLFDVKGDFFPEKQRI	237	
Qy	231	YKONETLDSNTSQIEVLYTTK	251	
Db	238	YSDNKTLTSTELHLDIYLYEK	258	

RESULT 12
E89969 enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucuma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: E89969
A>Status: preliminary
A:Molecule type: DNA
B:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT_Q99T46; GB:BA000018; PID:gl3701623; PIDN:BAB42916.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: seo
C:Superfamily: enterotoxin B

	Query Match	25.6%;	Score 338;	DB 2;	Length 260;
	Best Local Similarity	36.2%;	Pred. No. 8.4e-18;		
	Matches 96;	Conservative 42;	Mismatches 107;	Indels 20;	Gaps 9
Qy	1	MENKKVLKMWFFVLVTFLGLTISQEVFA-QQDDPDSQLHRSSLVK--NLQNIYFLYEG	57		
Db	1	MKNSKVMLN--VLLILMLIAICSYNNAYANEDPKIESLCKSSVDPIALHNIIDDTYN	58		
Qy	58	DPVTHENVKSV----DQLSRHDLIYN---VSG--PNYDKLATELKNQSMATLEKDKNDV	107		
Db	59	NRFT--TVKSVISTTEKTFDLPOLLPSKINWLDPGISAEFKDLKVFSSSAISKEFLGKTVD	116		
Qy	108	IYGVBYHLYLCENAEARSACIYGVGTNHEGNHLBIPKKIVVKVSDIGQSLSFDIETNK	167		

[illegible]

```

RESULT 13
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89969
C:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q99T49; GB:BA000018; PID:g13701619; PIDN:BAB42912.
A:Experimental source: strain N315
C:Genetics:
A:Gene: Ventr

```

Query Match	25.5%;	Score 337;	DB 2;	Length 136;
Best Local Similarity	49.6%;	Pred. No. 4.4e-18;		
Matches 67;	Conservative 22;	Mismatches 38;	Indels 8;	Gaps 2
Qy	125	RSACIYGGVTHNEGNHL-----EIPKKIVVKVSDIGSIQSLSFDETNNKQMTVAQELDYK	178	
Db	2	KKTCMYGGVTHDGNQDKNNSTONSHNLLIKVTEENRNSLSFDIPNNKNTAQEIDYK	61	
Qy	179	VRKYLTDNKKLYTNGPSKYETGYIKFIPKNKESFWDFEPPE--PEFTQSOKYILMYIKDNKT	236	
Db	62	VRNYLLKHKNLVYFNSSPYETGYIKFETGSGHSFWYDLMPESGKKFYPTPKYLLIYNDNKT	121	
Qy	237	LDSNTSQIEVYLTTK	251	
Db	122	VESKSIINVEHLTKK	136	

RESULT 14
 C89984
 enterotoxin P [imported] - *Staphylococcus aureus* (strain N315)
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: C89984
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui
 ma, A.; Mizutani-Yi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: UNIPROT:Q99SU3; GB:BA000018; PID:gi3701743; PIDN:BAB43036.
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sep
 C:Superfamily: enterotoxin B
 Query Match 25.4%; Score 336; DB 2; Length 260;

Query Match 25.4%; Score 336; DB 2; Length 260;

Qy	181	KYLTDNKQLYNGPSKYETGYIKETIPKNKZSFWDPEPEFTQSKYLYMIYKDNETLDSN	240
Db	180	KYLTDNKQLYNGPSKYETGYIKETIPKNKZSFWDPEPEFTQSKYLYMIYKDNETLDSN	239
Qy	241	TSQIEVYLTTK	251
Db	240	TSQIEVYLTTK	250

RESULT 6

ENSAB6

enterotoxin B precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004

C:Accession: S27360; A92065; S27240; A01815

R:Jones, C.L.; Khan, S.A.

J. Bacteriol. 166, 29-33, 1986

A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.

A:Reference number: S27360; MUID:86168029; PMID:3957869

A:Accession: S27360

A:Molecule type: DNA

A:Residues: 1-266 <ON>

A:Cross-references: UNIPROT:P01552; EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g1530

A:Experimental source: strain S6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3518-3525, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide

A:Reference number: A92065; MUID:71007902; PMID:5470821

A:Accession: A92065

A:Molecule type: protein

A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',

A:Experimental source: strain S-6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3511-3517, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition

A:Reference number: A92064; MUID:71007901; PMID:5470820

A:Contents: annotation; chymotryptic peptides

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3493-3510, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition

A:Reference number: A92063; MUID:71007900; PMID:5470819

A:Contents: annotation; tryptic peptides

R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunmery, D.A.; Bergdoll, M.S.

Biochemistry 4, 1011-1016, 1965

A:Title: Purification of staphylococcal enterotoxin B.

A:Reference number: A90548; MUID:66035792; PMID:4953912

A:Contents: annotation; biological source of protein

R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni

Eur. J. Biochem. 209, 823-828, 1992

A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B

A:Reference number: S27240; MUID:93049338; PMID:1425690

A:Accession: S27240

A:Molecule type: protein

A:Residues: 28-42; 128-148 <ALA>

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin; extracellular protein; toxin

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-286/Product: enterotoxin B #status experimental <MAT>

F:120-140/Disulfide bonds: #status experimental

Query Match 43.6%; Score 576.5; DB 1; Length 266;
Best Local Similarity 48.2%; Pred. No. 2.1e-35;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7

Qy	15	VLVTFGLGIS-QEYPA--QDDPDSQLHRSLSKVL--ONIFYLVEGDPVTHENKVSQD	70
Db	11	ILIFAILVLIVSTNTVLAEQPPKDEFLHHSKSTGLMENNKKVLYDDNHVSAINVKSIDQ	70
Qy	71	LRSHDLIYNVSGP--YYDKLTKTELKNGEMATLFRQKVDVIYGYEYHYHLCYLCENA----	123
Db	71	FLYFDLIYSKTKLGNYNVSEVFNKQDLADKYKDKTVDFVFGANYYYQCVFSKKTNDIN	130

[illegible]

RESULT 7

S11885
 enterotoxin C3 - *Staphylococcus aureus*
 C;Species: *Staphylococcus aureus*
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S11885
 R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
 Mol. Gen. Genet. 220, 329-333, 1990
 A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison with the enterotoxin C2 gene
 A;Reference number: S11885; MUID:90220508; PMID:2325627
 A;Accession: S11885
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-266 <HOV>
 A;Cross-references: UNIPROT:P23313; GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
 C;Superfamily: enterotoxin B

Query Match	41.7%	Score 551.5;	DB 2;	Length 266;
Best Local Similarity	46.1%;	Pred. No. 1.5e-33;		
Matches 117;	Conservative 46;	Mismatches 74;	Indels 17;	Gaps 8;
Qy	15	VLVTFGLTIS-QEVFAQQDPD--PSQLHRSS-LVRNLQNIFYLEGDPVTHENVKSVQD	70	
 :	:	: :: :::

Qy	71	LRSHDIYNVSG---	PNYDKKLTELKNQEMATL	FKKNVDI	GYVEYHL	CYLC--	ENAE	125
							:	
Db	71	FLAHLIYNI	DKKLXNYDKVKT	ELLNED	LAKKYK	DEVDV	DVGSNY	130
							:	
Qy	126	----	SACIYGGVTHRGSHLEIP--	KKIVVKS	IDGQLS	FDIETKN	QVTAQELDYK	179
							:	
	126	----	GGGGLVGGV	GGVGGV	GGVGGV	GGVGGV	GGVGGV	190
							:	

Qy	180	RKYLTDNKOLYATNGPSKYETGYIKFIPONKESWFQFPFPP	--EFTOSKYLMIWKDNETL	233
		:	:	
Db	191	RNFLKNGUUEFNSSPYETGYIKFIPONKESWFQFPFPP	--EFTOSKYLMIWKDNETL	250
		:	:	
Qy	238	DSNTSQIEVYLTTK	251	
		:	:	
Db	251	DSKSVKIEVHLTTK	264	
		:	:	

RESULT 8

A60114
 enterotoxin C-2 precursor - *Staphylococcus aureus*
 N;Alternate names: enterotoxin C-3 precursor
 C;Species: *Staphylococcus aureus*
 C;Date: 10-Nov-1992 #sequence revision 10-Nov-1992 #text_change 09-Jul-2004
 C;Accession: A60114; B60114; A33866
 R;Bohach, G.A.; Schlievert, P.M.
 Infect. Immun. 57, 2249-2252, 1989
 A;Title: Conservation of the biologically active portions of staphylococcal
 A;Reference number: A60114; PMID:89277549; PMID:2543637
 A;Accession: A60114
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-266 <BOH>
 A;Cross-references: UNIPROT:P34071
 A;Accession: B60114
 A;Molecule type: protein

A;Residues: 1-236 <NEA>
A;Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A;Experimental source: strain MGAS251 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18788
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEZ>
A;Cross-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A;Experimental source: strain MGAS256 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18790
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEY>
A;Cross-references: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A;Experimental source: strain MGAS285 isolate Colorado unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18792
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEO>
A;Cross-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18795
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEH>
A;Cross-references: EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18799
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NES>
A;Cross-references: EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID:g47326
A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18800
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA2>
A;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 93.3%; Score 1234; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 5.4e-84; Mismatches 0; Indels 0; Gaps 0;
Matches 234; Conservative 0;

QY 9 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVSGPNYDKLTTELKQEMATLTKDNVDIYGVYYHLCYLCENARSAC 128
Db 61 DQLLSHDLIYVSGPNYDKLTTELKQEMATLTKDNVDIYGVYYHLCYLCENARSAC 120

QY 129 IYGGVTNHEGHNHLEIPKKIYVVKVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNKQ 188
Db 121 IYGGVTNHEGHNHLEIPKKIYVVKVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNKQ 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEPFTQSKYLMYKONETLDSNTSQI 244
Db 181 LYTNGPSKYETGYIKFIPKNKESFWDFPPEPFTQSKYLMYKONETLDSNTSQI 236

RESULT 4
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes
A;Variety: strain MGAS262 isolate California

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: S18789
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene enco
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18789
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEU>
A;Cross-references: UNIPROT:Q54696; EMBL:X61573; NID:g47303; PIDN:CAA43771.1; PID:g4730
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 83.9%; Score 1109; DB 2; Length 236;
Best Local Similarity 88.6%; Pred. No. 9.1e-75;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 9 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVSGPNYDKLTTELKQEMATLTKDNVDIYGVYYHLCYLCENARSAC 128
Db 61 DQLLSHDLIYVSGPNYDKLTTELKQEMATLTKDNVDIYGVYYHLCYLCENARRAC 120

QY 129 IYGGVTNHEGHNHLEIPKKIYVVKVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNKQ 188
Db 121 IYGGVTNHEGHNHLEIPKKIYVVKVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNKQ 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEPFTQSKYLMYKONETLDSNTSQI 244
Db 181 LYTNGPSKYETGYIKFISDKETFWDFPPEPFTQSKYLMYKONETLDSNTSQI 236

RESULT 5
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N;Alternate names: scarlet fever toxin; SPE type A (speA)
C;Species: Streptococcus sp.
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A26152
R;Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to St
A;Reference number: A26152; MUID:86284313; PMID:3526093
A;Accession: A26152
A;Molecule type: DNA
A;Residues: 1-250 <JOH>
A;Cross-references: UNIPROT:P08095
C;Superfamily: enterotoxin B
C;Keywords: exotoxin

Query Match 81.4%; Score 1075.5; DB 1; Length 250;
Best Local Similarity 83.7%; Pred. No. 2.9e-72;
Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;

QY 1 MNNKKVLKQWFFVFLVTFGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPV 60
Db 1 MNNKEVLKQWFFVFLMKFLGLTILPKGICSTRPSPQLORSNLVTKFIYIFFRVTVL 60

QY 61 THENVKSVDQLRSHDLIYVSGPNYDKLTTELKQEMATLTKDNVDIYGVYYHLCYLC 120
Db 61 THENVKSVDQLLSHDLIYVSGPNYDKLTTELKQEMATLTKDNVDIYGVYYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNHLEIPKKIYVVKVSDIGIQLSFDIETNKKMVTQAQELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGHNHLEIPKKIYVVKVSDIGIQLSFDIETNKKMVTQAQELDYKVR 179

A;Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18797
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEH>
A;Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
A;Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18800
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-228 <NES>
A;Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328
A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA; speA1
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 99.5%; Score 1315; DB 1; Length 251;
Best Local Similarity 99.8%; Pred. No. 6.1e-90;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNKKVLKQWFFVLVTFGLGTISQEVFAQQDDPSQLHRSLSVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKQWFFVLVTFGLGTISQEVFAQQDDPSQLHRSLSVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTAKLNQEMATLFDKNVDIYGVVEYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTAKLNQEMATLFDKNVDIYGVVEYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNLETPKKIVVKVSDIGTQSISFDIETNKKMVTAGELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGHNLETPKKIVVKVSDIGTQSISFDIETNKKMVTAGELDYKVR 180

QY 181 KYLTDNKQLYNTGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLIYKDNETLDSN 240
DB 181 KYLTDNKQLYNTGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLIYKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 2
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isol
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S18783; S18793; S18794; S18801; S18798
R;Nelson, K.; Schlievert, P.M.; Selaender, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18783
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEL>
A;Cross-references: EMBL:X61568; NID:g47289; PIDN:CAA43766.1; PID:g47290
A;Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18793
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA>
A;Cross-references: EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: September 17, 2005, 01:00:14 ; Search time 18.153 Seconds
(without alignments)
1330.382 Million cell updates/sec
Title: US-10-002-784A-16
Perfect score: 1322
Sequence: 1 MNNKKVLKMWFFVLVTEL.....KDNETLDSNTSQIEVLLTK 251
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	99.5	231	1 S29659	exotoxin type A pr
2	1239	93.7	236	2 S18783	exotoxin type A pr
3	1234	93.3	236	2 S18786	exotoxin type A pr
4	1109	83.9	236	2 S18789	exotoxin A precurs
5	1075.5	81.4	250	1 A26152	streptococcal pyro
6	576.5	43.6	266	1 ENSAB6	enterotoxin B prec
7	551.5	41.7	286	2 S11885	enterotoxin C3 - S
8	549	41.5	266	2 A60114	enterotoxin C-2 pr
9	548	41.5	266	1 ENSAC1	enterotoxin C-1 pr
10	481	36.4	258	2 G89968	extracellular ente
11	340	25.7	258	2 A33953	enterotoxin D prec
12	338	25.6	260	2 E89969	enterotoxin Seq [i
13	337	25.5	136	2 A89969	enterotoxin YENT2
14	336	25.4	260	2 C89984	enterotoxin P [imp
15	311.5	23.6	258	2 H89968	enterotoxin Sen [i
16	308	23.3	257	2 A28179	enterotoxin A prec
17	307	23.2	257	2 A28664	extracellular ente
18	305.5	23.1	240	2 G89991	extracellular ente
19	264	20.0	239	2 D89969	enterotoxin SEM [i
20	251.5	19.0	242	2 C89969	extracellular ente
21	211	16.0	235	2 A30509	exotoxin C precurs
22	174	13.2	133	2 B89969	exotoxin Yent1
23	129.5	9.8	221	2 D89807	exotoxin 11 [impor
24	128	9.7	137	2 A89942	hypothetical prote
25	125	9.5	227	2 C89808	exotoxin 15 [impor
26	114	8.6	232	2 F89807	exotoxin 13 [impor
27	114	8.6	234	2 C89807	exotoxin 10 [impor
28	111	8.4	234	2 B89992	toxic shock syndro
29	111	8.4	292	2 B89807	exotoxin 9 [impor

30	109.5	8.3	825	2 H82885	hypothetical prote
31	109	8.2	234	1 XCSAS1	toxic shock syndro
32	108.5	8.2	231	2 H89806	exotoxin 7 [impor
33	108.5	8.2	596	2 E96935	FUSION, methionine
34	108	8.2	434	2 T28342	ORF MSV181 hypothe
35	108	8.2	493	2 G90604	hypothetical prote
36	105.5	8.0	1790	2 S67593	transport protein
37	105	7.9	770	2 B48910	desmocollin 1b pre
38	105	7.9	824	2 A48910	desmocollin 1a pre
39	105	7.9	840	2 I37281	Dsc1a precursor -
40	105	7.9	894	2 I37282	Dsc1b precursor -
41	104.5	7.9	1367	2 T18466	hypothetical prote
42	104.5	7.9	1856	2 C95008	immunoglobulin A1
43	103.5	7.8	241	2 B89888	hypothetical prote
44	103.5	7.8	396	2 S09627	prnC protein - Esc
45	103	7.8	235	2 C97252	probable membrane

ALIGNMENTS

RESULT 1

S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N:Alternate names: erythrogenic toxin; scarlet fever toxin
C:Species: Streptococcus pyogenes phage T12
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R:Weeks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin)
A:Reference number: S29659; MUID:86166804; PMID:3514452
A:Accession: S29659
A:Molecule type: DNA
A:Residues: 1-251 <WE>
A:Cross-references: GB:U40453; EMBL:X61560; NID:gl877426; PIDN:AA43754.1; PID:gl877430
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Museer, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene enco
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18782
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288
A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigne
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18784
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEA>
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassign
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18785
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEZ>
A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294
A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned p
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18791
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18796
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEO>
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

Db 250 VDSKDVKIEVYLTK 264

RESULT 15

```

US-09-751-708A-10
; Sequence 10, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCES: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-10

```

Query Match	43.6%;	Score 576.5;	DB 10;	Length 266;
Best Local Similarity	48.2%;	Pred. No. 1.3e-41;		
Matches 123;	Conservative 38;	Mismatches 75;	Indels 19;	Gaps 7;
Qy	15	VLVTFGLTIS-QEVFA--QODPPSOIHRSSLVNLL-ONIFYLYEGDPVTHENVKSVQD	70	
Db	11	ILIFALIVISTPNVLAEQSDPKPDELHKSSKFTGLMENNKKVLYDDNNHVSAINVKSIDQ	70	
Qy	71	LRSHDLIYNSGP--NVDLKTLELKNQEWATLFKDKNDVIYGVVEYVHLVCYLCENA----	123	
Db	71	FLIFDILLIYSIKDTKLGNIDNVRVEFKNGLADKYKDYVDFVGANYIYQYFSFKKTNDIN	130	
Qy	124	-----ERSACITYGVTNHEGNHLEIPKKIVVKVSDIGTQSLSFDIETNKKMVTQAELDYK	178	
Db	131	SHQTDREKTKCMYGGVTEHNGNQLDKYRSITVRVEFDGKNLLSFDVQTNKKVVTQAELDYL	190	
Qy	179	VRKYLTDNKKLYTNGPSKYETGYIKFIIPKNKESFWDFPFPEP--EFTQSKYLMITYKONET	236	
Db	191	TRHYLVKNKKLYEPNNSPYETGYIKFI--ENENSFWYDMMWPAFGPKFQSKYLMYNDNKM	249	
Qy	237	LDSENTSQIEVYLTTK	251	
Db	250	VDSKDKVIEVYLTTK	264	

Search completed: September 17, 2005, 01:05:39
Job time : 79.8484 secs

THIS PAGE BLANK (USPTO)

```
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-937-758A-20

Query Match      81.4%; Score 1075.5; DB 17; Length 250;
Best Local Similarity 83.7%; Pred. No. 6.7e-85;
Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;

QY 1 MENNKKVLKMMFFVFLVLTGLTISQEVFAQQDDPPSQLHSSLVKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKMMFFVFLVLTGLTILPKGICSTRPKSPQSLRSLVLTGPKIYIFFMRVTLV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKNOEMATLFDKKNVDIYGVYHLCYLC 120
Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKNOEMATLFDKKNVDIYGVYHLCYLC 120

QY 121 ENAERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMVTAAQELDYKVR 180
Db 121 ENAERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMVTAAQELDYKVR 180

QY 181 KYLTNKKQLYTNGPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
Db 181 KYLTNKKQLYTNGPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
Db 240 TSQIEVYLTTK 250
```

```
RESULT 13
US-10-354-948-2
; Sequence 2, Application US/10354948
; Publication NO. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Potter, Terence A.
; Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2

Query Match      44.5%; Score 588; DB 15; Length 255;
Best Local Similarity 47.2%; Pred. No. 1.2e-42;
Matches 119; Conservative 41; Mismatches 76; Indels 16; Gaps 5;

QY 15 VLVTFLGLTISQEVFAQQDDPPSQLHSSLVKNLQNIYFLYEGDPVTHENVKSVQDQRS 73
Db 3 MITNLRLITIGNSMESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLY 62

QY 74 HDLIYNVSGP---NYDKLTELKNOEMATLFDKKNVDIYGVYHLCYLCNA----- 123
Db 63 FDLIYSIKDTKLGNDYDNRVFEKNKLADKYDKYDVDFGANYYYQCYFSKKTNDINSHQ 122

QY 124 --ERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMVTAAQELDYKVR 181
Db 123 TDKRKTCMYGGVTEHNGQLDKYRSITVRVFDGKNLLSFDVQTNKKVTAQELDYLTRH 182

QY 182 YLTNKKQLYTNGPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNETLDS 239
Db 183 YLVNKKLYEFNNSPYETGIYKFI-ENENSWYDMPAPGDKFDQSKYLMYNDNMVDS 241

QY 240 NTSQIEVYLTTK 251
Db 242 KDKVIEVYLTTK 253

RESULT 14
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: THERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-10

Query Match      43.6%; Score 576.5; DB 9; Length 266;
Best Local Similarity 48.2%; Pred. No. 1.3e-41;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS-QEVFA--QQDPPSPQLHSSLVKNL-QNIYFLYEGDPVTHENVKSVQD 70
Db 11 ILIFALILVISTPNVLAESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ 70

QY 71 LRSHDLIYNVSGP---NYDKLTELKNOEMATLFDKKNVDIYGVYHLCYLCNA---- 123
Db 71 FLYFDLIYSIKDTKLGNDYDNRVFEKNKLADKYDKYDVDFGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTHNEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMVTAAQELDYK 178
Db 131 SHQTDKRRKTCMYGGVTEHNGQLDKYRSITVRVFDGKNLLSFDVQTNKKVTAQELDY 190

QY 179 VRKYLTNKKQLYTNGPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNET 236
Db 191 TRHYLVNKKLYEFNNSPYETGIYKFI-ENENSWYDMPAPGDKFDQSKYLMYNDNM 249

QY 237 LDSNTSQIEVYLTTK 251
```

```

; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PR1
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20

```

Query Match	81.4%;	Score 1075.5;	DB 9;	Length 250;
Best Local Similarity	83.7%;	Pred. No. 6.7e-85;		
Matches 210;	Conservative 7;	Mismatches 33;	Indels 1;	Gaps 1;
Qy	1	MENNKKVLKQWFFVLVTLGLTISOEVFAQDDPPSQLHRSSLVKNLQNTIYFLYEGDPV	60	
Db	1	MENNKEVLKQWFFVLKMKFLGLTLPGKICSTRPKPSQLQRSLNVKTEPKIIVFFMRVTLV	60	
Qy	61	THENVKSVDOLRSHDLIYNVSGNYDKLTTELKNOEMATLFKDKNVDIYGYEYHLCVLC	120	
Db	61	THENVKSVDOLRSHDLIYNVSGNYDKLTTELKNOEMATLFKDKNVDIYGYEYHLCVLC	120	
Qy	121	ENERSACIYGGVTNHEGNHLEIPKIIVVKVSIIDGIIQSLSFDIETNKKWVTAQELDYYKR	180	
Db	121	ENERSACLYGGVTNHEGNHLEIPKIIVVKVSIIDGIIQSLSFDIEIQKN-GNCSRTISYTVR	179	
Qy	181	KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWOFFPEPEPTQSKYLMIKYDNETLDSN	240	
Db	180	KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWOFFPEPEPTQSKYLMIKYDNETLDSN	239	
Qy	241	TSQIEVYLTTK	251	
Db	240	TSQIEVYLTTK	250	

```

RESULT 10
US-09-751-708A-20
; Sequence 20, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-751-708A-20

```

	Query Match	81.4%;	Score 1075.5;	DB 10;	Length 250;
	Best local Similarity	83.7%;	Pred. No. 6.7e-85;		
	Matches 210; Conservative	7;	Mismatches 33;	Indels 1;	Gaps 1;
Qy	1	MENNKKVYLKXWFFVLVTFLGLTISQVFQAQQDDPSQLHRSSLSVKNIQNITFYLYEGDPV	60		
		: : :			
Db	1	MENNEKVLKXWFFVLWKFLGTLTLPKGICSTRPKPQLQRSNLVTKFIYIFPMRVTVL	60		
		: : :			
Qy	61	THENVKVDQLRSHDLIYNVSGPNYDKLTKELNQEAMATLFPKKNVDIYGVEYYHLCVYC	120		
		: : :			
Db	61	THENVKVDQLLSHDLIYNVSGPNYDKLTKELNQEAMATLFPKKNVDIYGVEYYHLCVYC	120		
		: : :			
Qy	121	ENAERSACIYGGVNTNHEGNHLEIPKKIIVKWVSIDGIOSLSPDIEETNKMWTAQELDYKVR	180		
		: : :			
Db	121	ENAERSACL YGVNTNHEGNHLEIPKKIIVKWVSIDGIOSLSPDIEIQIKN-GNCRSISTVTR	179		
		: : :			
Qy	181	KYLTDNKQLYTNGPSKYETGYIKFIPKNKSFWFDFFPEPFETQSXYLMYIKDNETLDSN	240		
		: : :			
Db	180	KYLTDNKQLYTNGPSKYETGYIKFIPKNKSFWFDFFPEPFETQSXYLMYIKDNETLDSN	239		
		: : :			

```

Qy      241  TSQIEVYLTK 251
      |||||
Db      240  TSQIEVYLTK 250

RESULT 11
US-10-428-817A-16
; Sequence 16, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-16

```

Query Match	81.4%;	Score 1075.5;	DB 16;	Length 250;
Best Local Similarity	83.7%;	Pred. No. 6.7e-85;		
Matches 210;	Conservative 7;	Mismatches 33;	Indels 1;	Gaps 1
Qy	1	MENNKKVLLKKMVFVVLVTFGLGTISQEVFAQDDPPSQLHRSSLLKQNLQNIYFLYEGDPV	60	
Db	1	MENNKEVLLKKMVFVLMKFLGLTILPKGICSTRPKPSQLQRSNLVKTFKIYIFFMRVTLV	60	
Qy	61	THENVKSVQDLRSHDLJLYNVSGPNYDKLTKELKQEMATLFDKQKVDJYGVBYHYHLCYLC	120	
Db	61	THENVKSVQDLSHDLJLYNVSGPNYDKLTKELKQEMATLFDKQKVDJYGVBYHYHLCYLC	120	
Qy	121	ENASRSACIYGGVNTNHEGHNLEIPKIVVKVYSIDGIIQSLSPDIETNKKQMTVAQELDYKVR	180	
Db	121	ENASRSACIYGGVNTNHEGHNLEIPKIVVKVYSIDGIIQSLSPDIETNKKQMTVAQELDYKVR	179	
Qy	181	KYLTQNLQLYTNGSKYETGYIKIIPKNKESFWDFDFPEPEFTQSKYLMYKQNETLDSN	240	
Db	180	KYLTQNLQLYTNGSKYETGYIKIIPKNKESFWDFDFPEPEFTQSKYLMYKQNETLDSN	239	
Qy	241	TSQIEVYLTTK	251	
Db	240	TSQIEVYLTTK	250	

RESULT 12
US-10-937-758A-20
; Sequence 20, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884

```
; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-308-830-13

Query Match      98.9%; Score 1308; DB 9; Length 251;
Best Local Similarity 99.2%; Pred. No. 4.8e-105;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENNKKVLKMMFFVLVTLGLTISOEVPAQODPPSQLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKMMFFVLVTLGLTISOEVPAQODPPSQLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENKVSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKKNVDIYGVYHLCYLC 120
DB 61 THENKVSVDQLRSHDLIYNVSGPNYDKLTELKQEMATLFDKKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGVVTHNEGNHLEIPKKIVVKSIDGQSLSPDIETNKKQWTAQELDLYKVR 180
DB 121 ENAERSACIYGVVTHNEGNHLEIPKKIVVKSIDGQSLSPDIETNKKQWTAQELDLYKVR 180
QY 181 KYLTNKKQWTAQELDLYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 240
DB 181 KYLTNKKQWTAQELDLYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 7
US-10-002-784A-26
; Sequence 26, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match      85.9%; Score 1136; DB 14; Length 220;
Best Local Similarity 98.2%; Pred. No. 3.2e-90;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 31 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90
DB 2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
QY 91 ELKQEMATLFDKKNVDIYGVYHLCYLCENASRSACIYGVVTHNEGNHLEIPKKIVVK 150
DB 62 ELKQEMATLFDKKNVDIYGVYHLCYLCENASRSACI -GGVTNREGNHLEIPKKIVVK 120
QY 151 VSIDGQSLSPDIETNKKQWTAQELDLYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 210
DB 121 VSIDGQSLSPDIETNKKQWTAQELDLYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTTK 251
DB 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT -QIEVYLTTK 220

RESULT 9
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
```

Db 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSDIGIQSLSFDTETNKKMVTQAELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKNDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKNDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 4

US-10-428-817A-163
; Sequence 163, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes

US-10-428-817A-163

Query Match 99.5%; Score 1315; DB 16; Length 251;
Best Local Similarity 99.8%; Pred. No. 1.2e-105;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVFLVTLGLTISQEVFAQDDPPSQHLRSSLVKNLQNIYFLYEGDPV 60
Db 1 MNNKKVLKKMVFVFLVTLGLTISQEVFAQDDPPSQHLRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
Db 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSFDTETNKKMVTQAELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSFDTETNKKMVTQAELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKNDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKNDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 5

US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:

; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

Query Match 98.9%; Score 1308; DB 8; Length 251;
Best Local Similarity 99.2%; Pred. No. 4.8e-105;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVFLVTLGLTISQEVFAQDDPPSQHLRSSLVKNLQNIYFLYEGDPV 60
Db 1 MNNKKVLKKMVFVFLVTLGLTISQEVFAQDDPPSQHLRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
Db 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSFDTETNKKMVTQAELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSFDTETNKKMVTQAELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKNDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKNDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 6

US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997


```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match 100.0%; Score 1322; DB 8; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.9e-106;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLVTLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKQVFFVLVTLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIQSLSFDIETNKKMVTAAQELDVKVR 180
Db 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIQSLSFDIETNKKMVTAAQELDVKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 2
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match 100.0%; Score 1322; DB 14; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.9e-106;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLVTLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKQVFFVLVTLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIQSLSFDIETNKKMVTAAQELDVKVR 180
```

```
Db 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIQSLSFDIETNKKMVTAAQELDVKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 3
US-10-767-687-16
; Sequence 16, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

Query Match 100.0%; Score 1322; DB 17; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.9e-106;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLVTLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKQVFFVLVTLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIQSLSFDIETNKKMVTAAQELDVKVR 180
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
Run on: September 17, 2005, 00:44:58 ; Search time 77.8484 Seconds
(without alignments)
1305.574 Million cell updates/sec

Title: US-10-002-784A-16
Perfect score: 1322
Sequence: 1 MENNKVLKMWFFVLVTFPL.....KDNELDSNTSIOIEVILTK 251
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues
Total number of hits satisfying chosen parameters: 1812044
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				Published Applications AA.*			
1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*			1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*		
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*			2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*		
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*			3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*		
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*			4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*		
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*			5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*		
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*			6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*		
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*			7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*		
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*			8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*		
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*			9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*		
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*			10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*		
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*			11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*		
12:	/cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*			12:	/cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*		
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*			13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*		
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*			14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*		
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*			15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*		
16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*			16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*		
17:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*			17:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*		
18:	/cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*			18:	/cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*		
19:	/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*			19:	/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*		
20:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*			20:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*		
21:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*			21:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*		
22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*			22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Match	Length	ID	Description		
1	1322	100.0	251	8	US-08-882-431-16	Sequence 16, Appl	
2	1322	100.0	251	14	US-10-002-784A-16	Sequence 16, Appl	
3	1322	100.0	251	17	US-10-767-687-16	Sequence 16, Appl	
4	1315	99.5	251	16	US-10-428-817A-163	Sequence 163, App	
5	1308	98.9	251	8	US-08-973-391A-13	Sequence 13, Appl	
6	1308	98.9	251	9	US-09-308-830-13	Sequence 26, Appl	
7	1136	85.9	220	14	US-10-002-784A-26	Sequence 27, Appl	
8	1136	85.9	468	14	US-10-002-784A-27	Sequence 20, Appl	
9	1075.5	81.4	250	9	US-09-870-759-20	Sequence 20, Appl	
10	1075.5	81.4	250	10	US-09-751-708A-20	Sequence 16, Appl	
11	1075.5	81.4	250	16	US-10-428-817A-16		

12	1075.5	81.4	250	17	US-10-937-758A-20	Sequence 20, Appl
13	588	44.5	255	15	US-10-354-948-2	Sequence 2, Appl
14	576.5	43.6	266	9	US-09-870-759-10	Sequence 10, Appl
15	576.5	43.6	266	10	US-09-751-708A-10	Sequence 10, Appl
16	576.5	43.6	266	16	US-10-428-817A-6	Sequence 6, Appl
17	576.5	43.6	266	17	US-10-937-758A-10	Sequence 10, Appl
18	576	43.6	239	9	US-09-150-947B-12	Sequence 12, Appl
19	576	43.6	239	14	US-10-172-425B-12	Sequence 12, Appl
20	575	43.5	266	14	US-10-151-336-8	Sequence 8, Appl
21	574	43.4	238	16	US-10-428-817A-183	Sequence 183, App
22	567.5	42.9	266	14	US-10-002-784A-6	Sequence 6, Appl
23	567.5	42.9	266	17	US-10-767-687-6	Sequence 6, Appl
24	563	42.6	239	14	US-10-002-784A-10	Sequence 10, Appl
25	563	42.6	239	17	US-10-767-687-10	Sequence 10, Appl
26	558.5	42.2	266	14	US-10-002-784A-8	Sequence 8, Appl
27	558.5	42.2	266	17	US-10-767-687-8	Sequence 8, Appl
28	558	42.2	239	8	US-08-882-431-10	Sequence 10, Appl
29	553	41.8	266	8	US-08-882-431-14	Sequence 14, Appl
30	553	41.8	266	14	US-10-002-784A-14	Sequence 14, Appl
31	553	41.8	266	17	US-10-767-687-14	Sequence 14, Appl
32	551.5	41.7	266	16	US-10-428-817A-186	Sequence 186, App
33	549	41.5	265	8	US-08-882-431-6	Sequence 6, Appl
34	548	41.5	266	9	US-09-870-759-12	Sequence 12, Appl
35	548	41.5	266	10	US-09-751-708A-12	Sequence 12, Appl
36	548	41.5	266	16	US-10-428-817A-8	Sequence 8, Appl
37	548	41.5	266	17	US-10-937-758A-12	Sequence 12, Appl
38	547	41.4	240	17	US-10-923-324-4	Sequence 4, Appl
39	545	41.2	239	16	US-10-428-817A-185	Sequence 185, App
40	544	41.1	240	17	US-10-923-324-1	Sequence 1, Appl
41	542	41.0	265	8	US-08-882-431-8	Sequence 8, Appl
42	536	40.5	240	17	US-10-923-324-5	Sequence 5, Appl
43	535	40.5	240	17	US-10-923-324-3	Sequence 3, Appl
44	533	40.3	240	17	US-10-923-324-6	Sequence 6, Appl
45	532	40.2	240	17	US-10-923-324-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-882-431-16
; Sequence 16, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army WMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:

```
XX (MINU ) UNIV MINNESOTA.
XX
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page; 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX animals against wild type SPE-A and to treat cancer and streptococcal
XX toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX myositis, fascitis and liver damage. The neutralising Ab is preferably
XX administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and uterine
XX cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX cell lymphoma cells. N.B. Sequence not given in the specification, but
XX constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX Sequence 251 AA;
SQ
Query Match          98.2%; Score 1298; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. NO. 4.9e-109;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MENNKKVLKKMVFVFLVTLGLTISOEVFAQQDDPPSQLRSSLVKKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKKMVFVFLVTLGLTISOEVFAQQDDPPSQLRSSLVKKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTQEMATLFDKKNVDIYGVYHLCYL 120
Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTQEMATLFDKKNVDIYGVYHLCYL 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKIVVKVSDIGIQSLSPDIETNKKMVTQAQELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGNHLEIPKIVVKVSDIGIQSLSPDIETNKKMVTQAQELDYKVR 180
QY 181 KYLTQNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSN 240
Db 181 KYLTQNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251
```

Search completed: September 17, 2005, 01:09:41
Job time : 84.0376 secs

CC	toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
XX	
SQ	Sequence 251 AA;
	Query Match 98.3%; Score 1299; DB 2; Length 251; Best Local Similarity 98.4%; Pred.No. 3.9e-109; Matches 247; Conservative 2; Mismatches 2; Indels 0; Gaps 0
QY	1 MENNKKVLKMWFFVFLVTFGLTISQEVEFAQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPV 60
DB	1 MENNKKVLKMWFFVFLVTFGLTISQEVEFAQQDDPPSQLHRSLSLVKNLQDIYFLYEGDPV 60
QY	61 THENVKSDQLRSHDLIYNVSGPNVDKLTELKNQEMATLFKDKNVDIIYGVEYYHLCYLC 120
DB	61 THENVKSDQLLSHHLLIYNVSGPNVDKLTELKNQEMATLFKDKNVDIIYGVEYYHLCYLC 120
QY	121 ENAERSACIYGGVTNHGHNLEIPKKIVVKVISIDGIQSLSFDIETNKQWTAQELDYKVR 180
DB	121 ENAERSACIYGGVTNHGHNLEIPKKIVVKVISIDGIQSLSFDIETNKQWTAQELDYKVR 180
QY	181 KYLTDNKOLYNGPSKYETGYIKFIPKNKESFPWFDFPPEPTQSKYLMIYKDNETLDSN 240
DB	181 KYLTNEQLYNGPSKYETGYIKFIPKNKESFPWFDFPPEPTQSKYLMIYKDNETLDSN 240
QY	241 TSQIEVLYTTK 251
DB	241 TSQIEVLYTTK 251
RESULT 15	
ID	AAM12153 standard; protein; 251 AA.
XX	AA
AC	AAM12153;
XX	
DT	04-NOV-1997 (first entry)
XX	
DE	Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
KW	Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW	protection; treatment; cancer; neutralising antibody;
KW	streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW	hypotension; group A streptococcal infection; myositis; fascitis;
KW	liver damage; T cell; lymphoma; ovarian; uterine.
OS	Streptococcus pyogenes.
OS	Synthetic.
FH	Key Location/Qualifiers
FT	Peptide 1..30 /label= sig_peptide
FT	Peptide 31..251 /label= mat_peptide
FT	Misc-difference 120 /note= "wild type Cys replaced by Ser"
XX	
FN	WO9640930-A1.
XX	
PD	19-DEC-1996.
XX	
PF	07-JUN-1996; 96WO-US010252.
PR	07-JUN-1995; 95US-00480261.

```
XX 04-NOV-1997 (first entry)
XX Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.
DE Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW Streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fascitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX Streptococcus pyogenes.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 46
FT /note= "wild type Lys replaced by Asn"
XX
XX WO9640930-A1.
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010252.
XX
XX 07-JUN-1995; 95US-00480261.
XX (MINU ) UNIV MINNESOTA.
XX
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page; 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX animals against wild type SPE-A and to treat cancer and streptococcal
XX toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX myositis, fascitis and liver damage. The neutralising Ab is preferably
XX administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and uterine
XX cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX cell lymphoma cells. N.B. Sequence not given in the specification, but
XX constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX Sequence 251 AA;
XX
XX Query Match 98.6%; Score 1303; DB 2; Length 251;
XX Best Local Similarity 98.8%; Pred. No. 1.7e-109;
XX Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MENNKKVLKMPFFVLVTLGLTISOEVFAQQDPDPSQLHRSLSLVKNLQNIYFLVYEGDVP 60
XX
XX 1 MENNKKVLKMPFFVLVTLGLTISOEVFAQQDPDPSQLHRSLSLVNQLNIYFLVYEGDVP 60
XX
XX 61 THENVKSVQDLRSHDLIYVNGSPNYDKLTTELKNQEMATLFDKDNVDIYGVYHYHLCYLC 120
XX
XX 61 THENVKSVQDLRSHDLIYVNGSPNYDKLTTELKNQEMATLFDKDNVDIYGVYHYHLCYLC 120
XX
XX 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDGISOISLFDIETNKKMWTQAQLDYKVR 180
XX
XX 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDGISOISLFDIETNKKMWTQAQLDYKVR 180
XX
QY 181 KYLTDNKQLYTNQPSKYETGYIKFIPKNKGSFWDFPEPEFTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNQPSKYETGYIKFIPKNKGSFWDFPEPEFTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVLVLTTK 251
DB 241 TSQIEVLVLTTK 251
RESULT 13
AAW12147
ID AAW12147 standard; protein; 251 AA.
XX
XX AC AAW12147;
XX
XX 04-NOV-1997 (first entry)
XX Streptococcus pyogenes Streptococcal toxin A mutant Asn20Aasp.
XX
XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW Streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fascitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX Streptococcus pyogenes.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 50
FT /note= "wild type Asn replaced by Asp"
XX
XX WO9640930-A1.
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010252.
XX
XX 07-JUN-1995; 95US-00480261.
XX (MINU ) UNIV MINNESOTA.
XX
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.
XX
XX Claim 5; Page; 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX animals against wild type SPE-A and to treat cancer and streptococcal
XX toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX myositis, fascitis and liver damage. The neutralising Ab is preferably
XX administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and uterine
XX cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX cell lymphoma cells. N.B. Sequence not given in the specification, but
XX constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX Sequence 251 AA;
XX
XX Query Match 98.6%; Score 1303; DB 2; Length 251;
XX Best Local Similarity 98.8%; Pred. No. 1.7e-109;
```


CC and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes
 CC neutralising antibodies (Ab) to be produced, which may be used to
 CC ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal
 CC infection, myositis, fascitis and liver damage. The neutralising Ab is
 CC preferably administered in conjunction with antibiotic therapy. The
 CC mutant SPE-A is especially useful for treating T cell lymphomas, and
 CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
 CC selectively toxic to T cell lymphoma cells
 XX
 SQ Sequence 251 AA;

Query Match 98.9%; Score 1308; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 6e-110;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MENNKKVLKKMVFVLTFLGLTISQEVFAQDDPPSOLHRSLLVKNLQNIYFLYEGDPV 60
 Db 1 MENNKKVLKKMVFVLTFLGLTISQEVFAQDDPPSOLHRSLLVKNLQNIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGVEYHLCYLC 120
 Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGVEYHLCYLC 120
 QY 121 ENAERSACIYGGVTHNHEGNHLEIPKIVVKVSIIDGSIQSLSPDIETNKKMVTQAQLDYKVR 180
 Db 121 ENAERSACIYGGVTHNHEGNHLEIPKIVVKVSIIDGSIQSLSPDIETNKKMVTQAQLDYKVR 180
 QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 QY 241 TSQIEVYLTTK 251
 Db 241 TSQIEVYLTTK 251

RESULT 9
 AAW59780
 ID AAW59780 standard; protein; 251 AA.
 AC AAW59780;
 DT 12-OCT-1998 (first entry)
 DE Amino acid sequence of Streptococcus pyogenes exotoxin A.
 XX
 KW SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
 KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
 KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;
 KW uterine cancer.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO9824911-A2.
 XX
 PD 11-JUN-1998.
 XX
 PF 05-DEC-1997; 97WO-US022228.
 XX
 PR 06-DEC-1996; 96US-0032930P.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 XX
 DR WPI; 1998-333330/29.
 XX
 DR N-P8DB; AAV41593.
 XX
 PT New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or
 PT treatment of streptococcal infection or toxic shock syndrome.
 XX
 PS Disclosure; Fig 3; 95pp; English.
 XX

CC This is the amino acid sequence of the Streptococcus pyogenes exotoxin A
 CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1
 CC aa change and is nonlethal compared with a protein to wild type SPE-A
 CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies
 CC that neutralise wild type SPE-A toxin activity. The toxins can be used in
 CC vaccines and therapeutics to generate a protective immune response
 CC against streptococcal infection. They can be used to protect against the
 CC development of streptococcal toxic shock syndrome (STSS). In addition,
 CC the toxins can be used for treating animals with symptoms of
 CC streptococcal infection or STSS and in methods for stimulating T cell
 CC proliferation and in the treatment of cancer. In particular they can be
 CC used for treating T cell lymphomas, and ovarian and uterine cancer
 XX
 SQ Sequence 251 AA;

Query Match 98.9%; Score 1308; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 6e-110;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MENNKKVLKKMVFVLTFLGLTISQEVFAQDDPPSOLHRSLLVKNLQNIYFLYEGDPV 60
 Db 1 MENNKKVLKKMVFVLTFLGLTISQEVFAQDDPPSOLHRSLLVKNLQNIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGVEYHLCYLC 120
 Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGVEYHLCYLC 120
 QY 121 ENAERSACIYGGVTHNHEGNHLEIPKIVVKVSIIDGSIQSLSPDIETNKKMVTQAQLDYKVR 180
 Db 121 ENAERSACIYGGVTHNHEGNHLEIPKIVVKVSIIDGSIQSLSPDIETNKKMVTQAQLDYKVR 180
 QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 QY 241 TSQIEVYLTTK 251
 Db 241 TSQIEVYLTTK 251

RESULT 10
 AAW12154
 ID AAW12154 standard; protein; 251 AA.
 AC AAW12154;
 DT 04-NOV-1997 (first entry)
 XX
 DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.
 XX
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
 KW protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
 KW hypotension; group A streptococcal infection; myositis; fascitis;
 KW liver damage; T cell; lymphoma; ovarian; uterine.
 XX
 OS Streptococcus pyogenes.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..30
 FT /label= sig_peptide
 FT Peptide 31..251
 FT /label= mat_peptide
 FT Misc-difference 225
 FT /note= "wild type Ser replaced by Ala"
 XX
 PN WO9640930-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010252.
 XX

KW Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
KW gene therapy.

XX Streptococcus pyogenes.

XX Key Location/Qualifiers

FT Peptide 1..29

FT /label= signal_peptide

FT Protein 30..251

FT /note= "S. pyogenes mature SpeA protein"

XX WO2003056015-A1.

XX 10-JUL-2003.

XX 26-NOV-2001; 2001WO-US046540.

XX 26-NOV-2001; 2001US-00002784.

XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX Ulrich RG;

XX WPI; 2003-492125/46.

XX N-PSDB; AAD56771.

XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.

XX Claim 9; Page 130-131; 141pp; English.

XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is Streptococcus pyogenes
XX pyrogenic exotoxin A (SpeA) protein. This sequence is used in the
XX invention

XX Sequence 251 AA;

Query Match 100.0%; Score 1322; DB 7; Length 251;

Best Local Similarity 100.0%; Pred. No. 3.3e-111;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVFLVTLTISQEVFAQQDDPPSOLHRSLVKNLQNIYFLYEGDPV 60

Db 1 MNNKKVLKKMVFVFLVTLTISQEVFAQQDDPPSOLHRSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFKDKNVDIYGVYYHLCYLC 120

Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFKDKNVDIYGVYYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGNHLEIPKIVVKVSDIGISQISLFDIETNKKMVTQAQELDYKVR 180

Db 121 ENAERSACIYGGVTNHEGNHLEIPKIVVKVSDIGISQISLFDIETNKKMVTQAQELDYKVR 180

QY 181 KYLTNDKQLYTGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240

Db 181 KYLTNDKQLYTGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLITTK 251

Db 241 TSQIEVYLITTK 251

RESULT 6

ABU62460

ID ABU62460 standard; protein; 251 AA.

XX AC

XX ABU62460;

XX

DT 27-AUG-2003 (first entry)

DE Streptococcus pyrogenic toxin a L42A mutant.

XX SPEa; streptococcus pyrogenic enterotoxin a; mutant; vaccine; mutein;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.

OS Streptococcus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..30

FT /label= signal_peptide

FT Protein 31..251

FT /label= Mature_SPEa_L42R

FT Misc-difference 72

FT /note= "Wild-type Leu substituted by Ala"

XX US2003036644-A1.

XX 20-FEB-2003.

XX 26-NOV-2001; 2001US-00002784.

XX 25-JUN-1997; 97US-00882431.

XX 01-SEP-1998; 98US-00144776.

XX (ULRI/) ULRICH R G.

XX Ulrich RG;

XX WPI; 2003-492125/46.

XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.

XX Example 13; Page; 68pp; English.

XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified altered superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection, an
XX antiserum isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX SEB, SEB1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX composition for treating or preventing bacterial infection. The present
XX sequence represents the L42A (with reference to the mature protein)
XX mutant of SPEa. Note: The present sequence is not shown in the
XX specification but was created by the indexer using the wild-type sequence
XX and the information in the specification

XX Sequence 251 AA;

Query Match 99.5%; Score 1316; DB 7; Length 251;

Best Local Similarity 99.6%; Pred. No. 1.1e-110;

Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVFLVTLTISQEVFAQQDDPPSOLHRSLVKNLQNIYFLYEGDPV 60

Db 1 MNNKKVLKKMVFVFLVTLTISQEVFAQQDDPPSOLHRSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFKDKNVDIYGVYYHLCYLC 120

```

PS Claim 17; Page 34-35; 50pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of streptococcal pyrogenic
CC exotoxin A
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNNKKVLKQWFFVLVTFGLTISQEVFAQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKQWFFVLVTFGLTISQEVFAQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYHYLCYLC 120
DB 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYHYLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIIDGSIQSLSPDIETNKKMWTAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIIDGSIQSLSPDIETNKKMWTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLIYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLIYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251
RESULT 4
ABU62331
ID ABU62331 standard; protein; 251 AA.
AC
XX ABU62331;
XX
DT 27-AUG-2003 (first entry)
XX
DE Streptococcus pyrogenic toxin a L42R mutant.
XX
KW SPEa; streptococcus pyrogenic enterotoxin a; mutant; vaccine; mutein;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Streptococcus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= signal_peptide
FT /label= Mature_SPEa_L42R
FT Misc-difference 72
FT /note= "Wild-type Leu substituted by Arg"
XX
XX US2003036644-A1.
XX
XX 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-00002784.
XX

```

```

PR 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-00144776.
XX
PA (ULRI/) ULRICH R G.
XX
PI Ulrich RG;
XX
XX WPI; 2003-492125/46.
DR N-PSDB; ACD28901.
XX
PT New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
PS Claim 9; Page 37-38; 68pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antisera isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the L42R (with reference to the mature protein)
CC mutant of SPEa
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNNKKVLKQWFFVLVTFGLTISQEVFAQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKQWFFVLVTFGLTISQEVFAQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYHYLCYLC 120
DB 61 THENVKVDQLRSHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVYHYLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIIDGSIQSLSPDIETNKKMWTAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIIDGSIQSLSPDIETNKKMWTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLIYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLIYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251
RESULT 5
AAE37683
ID AAE37683 standard; protein; 251 AA.
XX
XX AAE37683;
XX
XX 06-OCT-2003 (first entry)
XX
XX Streptococcus pyogenes pyrogenic exotoxin A (SPEa) protein.
XX

```

```

CC bacterial infections
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQDDPDPQSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQDDPDPQSOLHRSSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKNVDIYGVYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIIDGIQSLSFDIETNKKMVTQAQLDYKVR 180
DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIIDGIQSLSFDIETNKKMVTQAQLDYKVR 180

QY 181 KYLTDNKQLYTNGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 2
ID ABB79508 standard; protein; 251 AA.
XX
AC ABB79508;
XX
DT 23-SEP-2002 (first entry)
XX
DE Streptococcal pyrogenic exotoxin A vaccine SPEa42.
XX
KW Exotoxin A; SPEa; SPEa42; superantigen; antigen; toxin; vaccine;
KW attenuation; mutant; mutein.
XX
OS Streptococcus pyogenes.
XX
OS Synthetic.
XX
PN US6399332-B1.
XX
PD 04-JUN-2002.
XX
PF 01-SEP-1998; 98US-00144776.
XX
PR 25-JUN-1997; 97US-00882431.
XX
PA (USSA ) US SEC OF ARMY.
XX
XX
XX Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2002-546281/58.
XX
XX N-PSDB; ABN84229.
XX
XX Novel isolated and purified superantigen toxin DNA fragment which has
XX been genetically altered, useful for producing vaccine for treatment of
XX superantigen toxin-associated bacterial diseases.
XX
XX Disclosure; Col 63-65; 46pp; English.
XX
XX The present sequence is the protein sequence of Streptococcus pyogenes
XX vaccine SPEa42. The vaccine differs from the native SPEa sequence by
XX substitution of the leu-42 residue by Arg. This mutation is expected to
XX disrupt contact between the toxin and the HLA-DR receptor, reducing DRI
XX binding. SPEa42 can be expressed as a recombinant protein in Escherichia
XX coli as a secreted protein or as a cytoplasmic product. No indicators of
XX toxicity have been detected for the purified recombinant protein, and

```

```

CC vaccine studies demonstrate that SPEa42 is highly antigenic, inducing
CC protective immunity in a mouse animal model. The attenuated superantigen
CC can be used to protect against superantigen toxin infections. Methods of
CC producing and using altered superantigen toxins as vaccines, and in
CC diagnosis and therapy, are provided by the invention. A multivalent
CC vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1,
CC TSST-1 and SPEa is predicted to provide protective immunity against the
CC majority of bacterial superantigen toxins
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQDDPDPQSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQDDPDPQSOLHRSSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKNVDIYGVYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIIDGIQSLSFDIETNKKMVTQAQLDYKVR 180
DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIIDGIQSLSFDIETNKKMVTQAQLDYKVR 180

QY 181 KYLTDNKQLYTNGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 3
ABU10088
ID ABU10088 standard; protein; 251 AA.
XX
AC ABU10088;
XX
DT 11-AUG-2003 (first entry)
XX
DE Streptococcal pyrogenic exotoxin A.
XX
KW Pyrogenic exotoxin A; superantigen-associated bacterial infection;
KW superantigen toxin; vaccine.
XX
OS Streptococcus sp.
XX
PN US2003009015-A1.
XX
PD 09-JAN-2003.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX (ULRI/) ULRICH R G.
XX (OLSO/) OLSON M A.
XX (BAVA/) BAVARI S.
XX
XX Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2003-401542/38.
XX
XX N-PSDB; ACA61184.
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or I cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:47:53 ; Search time 82.0376 Seconds
(without alignments)
1183.322 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322

Sequence: 1 MNNKVKLVKKWFFVLVTF.....KDNETLDSNTSQIEVLLTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322	100.0	251	3 AAY70109	Streptococcus
2	1322	100.0	251	5 ABB79508	Streptococcus
3	1322	100.0	251	6 ABU10088	Streptococcus
4	1322	100.0	251	7 ABU62331	Streptococcus
5	1322	100.0	251	7 AAE37683	Streptococcus
6	1316	99.5	251	7 ABU62460	Streptococcus
7	1315	99.5	251	8 ADF89839	Streptococcus
8	1308	98.9	251	2 AAW12097	Streptococcus
9	1308	98.9	251	2 AAW59780	Amino acid
10	1305	98.7	251	2 AAW12154	Streptococcus
11	1304	98.6	251	2 AAW12146	Streptococcus
12	1303	98.6	251	2 AAW12150	Streptococcus
13	1303	98.6	251	2 AAW12147	Streptococcus
14	1299	98.3	251	2 AAW12148	Streptococcus
15	1298	98.2	251	2 AAW12153	Streptococcus
16	1298	98.2	251	2 AAW12151	Streptococcus
17	1298	98.2	251	2 AAW12152	Streptococcus
18	1293	97.8	251	2 AAW12149	Streptococcus
19	1288	97.5	250	2 AAW12145	Streptococcus
20	1288	97.4	251	2 AAW59798	Amino acid
21	1286	97.3	251	2 AAW59781	Amino acid
22	1170	88.5	221	4 AAB67344	Streptococcus
23	1164	88.0	221	2 AAR13209	Streptococcus
24	1164	88.0	221	2 AAR45017	Staphylococcus
25	1164	88.0	221	5 ABB76240	Staphylococcus

26	1136	85.9	220	7 ABU62334	Streptococcus
27	1136	85.9	220	7 AAE37687	Streptococcus
28	1136	85.9	468	7 ABU62335	Streptococcus
29	1136	85.9	468	7 AAE37684	Streptococcus
30	1131	85.6	220	7 AAE37689	S. pyogenes
31	1130	85.5	220	7 AAE37688	S. pyogenes
32	1130	85.5	468	7 AAE37691	S. pyogenes
33	1075.5	81.4	250	6 ABU79074	S. pyogenes
34	1075.5	81.4	250	7 ADF43300	Pyrogenic
35	588	44.5	255	2 AAW06737	Staphylococcus
36	576.5	43.6	266	6 ABU79069	S. aureus
37	576.5	43.6	266	7 ABG75015	S. aureus
38	576.5	43.6	266	7 ADF43290	Staphylococcus
39	576	43.6	239	2 AAW64647	Synthetic
40	575	43.5	266	3 AAY92319	Plant-opt
41	574.5	43.5	266	7 ABU62454	S. aureus
42	574	43.4	238	8 ADF89825	Staphylococcus
43	574	43.4	239	4 AAB67341	Staphylococcus
44	574	43.4	239	7 ABG75016	Unidentified
45	574	43.4	239	8 ADL14247	Wild type

ALIGNMENTS

RESULT 1

AAV70109

ID AAY70109 standard; protein; 251 AA.

XX AAY70109;

XX AC

XX 05-JUN-2000 (first entry)

XX Streptococcal pyrogenic exotoxin A (SPE-A).

XX Superantigen toxin; SAG; Streptococcal pyrogenic exotoxin A; SPE-A;
antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
cytostatic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;
diagnosis; treatment; superantigen-associated bacterial infection.

OS Streptococcus sp.

XX WO200009154-A1.

XX 24-FEB-2000.

XX 13-AUG-1998; 98WO-US016766.

XX 13-AUG-1998; 98WO-US016766.

XX (REED-) REED ARMY INST RES WALTER.

XX Ulrich RG, Olson MA, Bavari S;

XX WPI: 2000-224177/19.

XX N-PSDB; AAZ51112.

XX Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections.

XX Example 12; Page 94-95; 118pp; English.

XX The present amino acid sequence is the Streptococcal pyrogenic exotoxin A (SPE-A), a bacterial superantigen toxin (SAG), used for the formulation of SPE-A vaccine SPEA42. The coding region of this SAG toxin is altered by site directed mutagenesis, introducing L42R mutation, that results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SPE-A has antibacterial and cytostatic activity. This sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxins and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated